

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Darnell Jr., James E.
Schindler, Christian W.
Fu, Xian-Yuan
Wen, Zilong
Zhong, Zhong
- (ii) TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
SEQUENCES AND METHODS OF USE THEREOF
- (iii) NUMBER OF SEQUENCES: 25
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Klauber & Jackson
 - (B) STREET: 411 Hackensack Avenue
 - (C) CITY: Hackensack
 - (D) STATE: New Jersey
 - (E) COUNTRY: USA
 - (F) ZIP: 07601
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/212,185
 - (B) FILING DATE: 11-MAR-1994
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/980,498
 - (B) FILING DATE: 23-NOV-1992
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/854,296
 - (B) FILING DATE: 19-MAR-1992
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: WO US93/02569
 - (B) FILING DATE: 19-MAR-1993
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/126,588
 - (B) FILING DATE: 24-SEP-1993
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Jackson Esq., David A.
 - (B) REGISTRATION NUMBER: 26,742
 - (C) REFERENCE/DOCKET NUMBER: 600-1-073 CIP
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 201 487-5800
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 - (C) TELEX: 133521

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3268 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:
 (B) CLONE: HeLa

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 25..2577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ACTGCAACCC TAATCAGAGC CCAA ATG GCG CAG TGG GAA ATG CTG CAG AAT	51
Met Ala Gln Trp Glu Met Leu Gln Asn	
1 5	
CTT GAC AGC CCC TTT CAG GAT CAG CTG CAC CAG CTT TAC TCG CAC AGC	99
Leu Asp Ser Pro Phe Gln Asp Gln Leu His Gln Leu Tyr Ser His Ser	
10 15 20 25	
CTC CTG CCT GTG GAC ATT CGA CAG TAC TTG GCT GTC TGG ATT GAA GAC	147
Leu Leu Pro Val Asp Ile Arg Gln Tyr Leu Ala Val Trp Ile Glu Asp	
30 35 40	
CAG AAC TGG CAG GAA GCT GCA CTT GGG AGT GAT GAT TCC AAG GCT ACC	195
Gln Asn Trp Gln Glu Ala Ala Leu Gly Ser Asp Asp Ser Lys Ala Thr	
45 50 55	
ATG CTA TTC TTC CAC TTC TTG GAT CAG CTG AAC TAT GAG TGT GGC CGT	243
Met Leu Phe Phe His Phe Leu Asp Gln Leu Asn Tyr Glu Cys Gly Arg	
60 65 70	
TGC AGC CAG GAC CCA GAG TCC TTG TTG CTG CAG CAC AAT TTG CGG AAA	291
Cys Ser Gln Asp Pro Glu Ser Leu Leu Leu Gln His Asn Leu Arg Lys	
75 80 85	
TTC TGC CGG GAC ATT CAG CCC TTT TCC CAG GAT CCT ACC CAG TTG GCT	339
Phe Cys Arg Asp Ile Gln Pro Phe Ser Gln Asp Pro Thr Gln Leu Ala	
90 95 100 105	
GAG ATG ATC TTT AAC CTC CTT CTG GAA GAA AAA AGA ATT TTG ATC CAG	387
Glu Met Ile Phe Asn Leu Leu Leu Glu Glu Lys Arg Ile Leu Ile Gln	
110 115 120	
GCT CAG AGG GCC CAA TTG GAA CAA GGA GAG CCA GTT CTC GAA ACA CCT	435
Ala Gln Arg Ala Gln Leu Glu Gln Gly Glu Pro Val Leu Glu Thr Pro	
125 130 135	
GTG GAG AGC CAG CAA CAT GAG ATT GAA TCC CGG ATC CTG GAT TTA AGG	483
Val Glu Ser Gln Gln His Glu Ile Glu Ser Arg Ile Leu Asp Leu Arg	
140 145 150	
GCT ATG ATG GAG AAG CTG GTA AAA TCC ATC AGC CAA CTG AAA GAC CAG	531
Ala Met Met Glu Lys Leu Val Lys Ser Ile Ser Gln Leu Lys Asp Gln	
155 160 165	
CAG GAT GTC TTC TGC TTC CGA TAT AAG ATC CAG GCC AAA GGG AAG ACA	579
Gln Asp Val Phe Cys Phe Arg Tyr Lys Ile Gln Ala Lys Gly Lys Thr	
170 175 180 185	

CCC	TCT	CTG	GAC	CCC	CAT	CAG	ACC	AAA	GAG	CAG	AAG	ATT	CTG	CAG	GAA	627
Pro	Ser	Leu	Asp	Pro	His	Gln	Thr	Lys	Glu	Gln	Lys	Ile	Leu	Gln	Glu	
				190					195					200		
ACT	CTC	AAT	GAA	CTG	GAC	AAA	AGG	AGA	AAG	GAG	GTG	CTG	GAT	GCC	TCC	675
Thr	Leu	Asn	Glu	Leu	Asp	Lys	Arg	Arg	Lys	Glu	Val	Leu	Asp	Ala	Ser	
			205					210					215			
AAA	GCA	CTG	CTA	GGC	CGA	TTA	ACT	ACC	CTA	ATC	GAG	CTA	CTG	CTG	CCA	723
Lys	Ala	Leu	Leu	Gly	Arg	Leu	Thr	Thr	Leu	Ile	Glu	Leu	Leu	Leu	Pro	
		220					225					230				
AAG	TTG	GAG	GAG	TGG	AAG	GCC	CAG	CAG	CAA	AAA	GCC	TGC	ATC	AGA	GCT	771
Lys	Leu	Glu	Glu	Trp	Lys	Ala	Gln	Gln	Gln	Lys	Ala	Cys	Ile	Arg	Ala	
	235					240					245					
CCC	ATT	GAC	CAC	GGG	TTG	GAA	CAG	CTG	GAG	ACA	TGG	TTC	ACA	GCT	GGA	819
Pro	Ile	Asp	His	Gly	Leu	Glu	Gln	Leu	Glu	Thr	Trp	Phe	Thr	Ala	Gly	
250					255					260					265	
GCA	AAG	CTG	TTG	TTT	CAC	CTG	AGG	CAG	CTG	CTG	AAG	GAG	CTG	AAG	GGA	867
Ala	Lys	Leu	Leu	Phe	His	Leu	Arg	Gln	Leu	Leu	Lys	Glu	Leu	Lys	Gly	
				270					275					280		
CTG	AGT	TGC	CTG	GTT	AGC	TAT	CAG	GAT	GAC	CCT	CTG	ACC	AAA	GGG	GTG	915
Leu	Ser	Cys	Leu	Val	Ser	Tyr	Gln	Asp	Asp	Pro	Leu	Thr	Lys	Gly	Val	
			285					290					295			
GAC	CTA	CGC	AAC	GCC	CAG	GTC	ACA	GAG	TTG	CTA	CAG	CGT	CTG	CTC	CAC	963
Asp	Leu	Arg	Asn	Ala	Gln	Val	Thr	Glu	Leu	Leu	Gln	Arg	Leu	Leu	His	
		300					305					310				
AGA	GCC	TTT	GTG	GTA	GAA	ACC	CAG	CCC	TGC	ATG	CCC	CAA	ACT	CCC	CAT	1011
Arg	Ala	Phe	Val	Val	Glu	Thr	Gln	Pro	Cys	Met	Pro	Gln	Thr	Pro	His	
	315					320					325					
CGA	CCC	CTC	ATC	CTC	AAG	ACT	GGC	AGC	AAG	TTC	ACC	GTC	CGA	ACA	AGG	1059
Arg	Pro	Leu	Ile	Leu	Lys	Thr	Gly	Ser	Lys	Phe	Thr	Val	Arg	Thr	Arg	
330					335					340					345	
CTG	CTG	GTG	AGA	CTC	CAG	GAA	GGC	AAT	GAG	TCA	CTG	ACT	GTG	GAA	GTC	1107
Leu	Leu	Val	Arg	Leu	Gln	Glu	Gly	Asn	Glu	Ser	Leu	Thr	Val	Glu	Val	
				350					355					360		
TCC	ATT	GAC	AGG	AAT	CCT	CCT	CAA	TTA	CAA	GGC	TTC	CGG	AAG	TTC	AAC	1155
Ser	Ile	Asp	Arg	Asn	Pro	Pro	Gln	Leu	Gln	Gly	Phe	Arg	Lys	Phe	Asn	
			365					370					375			
ATT	CTG	ACT	TCA	AAC	CAG	AAA	ACT	TTG	ACC	CCC	GAG	AAG	GGG	CAG	AGT	1203
Ile	Leu	Thr	Ser	Asn	Gln	Lys	Thr	Leu	Thr	Pro	Glu	Lys	Gly	Gln	Ser	
		380					385					390				
CAG	GGT	TTG	ATT	TGG	GAC	TTT	GGT	TAC	CTG	ACT	CTG	GTG	GAG	CAA	CGT	1251
Gln	Gly	Leu	Ile	Trp	Asp	Phe	Gly	Tyr	Leu	Thr	Leu	Val	Glu	Gln	Arg	
	395					400					405					
TCA	GGT	GGT	TCA	GGA	AAG	GGC	AGC	AAT	AAG	GGG	CCA	CTA	GGT	GTG	ACA	1299
Ser	Gly	Gly	Ser	Gly	Lys	Gly	Ser	Asn	Lys	Gly	Pro	Leu	Gly	Val	Thr	
410					415					420					425	
GAG	GAA	CTG	CAC	ATC	ATC	AGC	TTC	ACG	GTC	AAA	TAT	ACC	TAC	CAG	GGT	1347
Glu	Glu	Leu	His	Ile	Ile	Ser	Phe	Thr	Val	Lys	Tyr	Thr	Tyr	Gln	Gly	
				430					435					440		
CTG	AAG	CAG	GAG	CTG	AAA	ACG	GAC	ACC	CTC	CCT	GTG	GTG	ATT	ATT	TCC	1395
Leu	Lys	Gln	Glu	Leu	Lys	Thr	Asp	Thr	Leu	Pro	Val	Val	Ile	Ile	Ser	
			445					450					455			

—AAC Asn	ATG Met	AAC Asn 460	CAG Gln	CTC Leu	TCA Ser	ATT Ile	GCC Ala 465	TGG Trp	GCT Ala	TCA Ser	GTT Val	CTC Leu 470	TGG Trp	TTC Phe	AAT Asn	1443
TTG Leu 475	CTC Leu	AGC Ser	CCA Pro	AAC Asn	CTT Leu	CAG Gln 480	AAC Asn	CAG Gln	CAG Gln	TTC Phe	TTC Phe 485	TCC Ser	AAC Asn	CCC Pro	CCC Pro	1491
AAG Lys 490	GCC Ala	CCC Pro	TGG Trp	AGC Ser	TTG Leu 495	CTG Leu	GGC Gly	CCT Pro	GCT Ala	CTC Leu 500	AGT Ser	TGG Trp	CAG Gln	TTC Phe	TCC Ser 505	1539
TCC Ser	TAT Tyr	GTT Val	GGC Gly	CGA Arg 510	GGC Gly	CTC Leu	AAC Asn	TCA Ser	GAC Asp 515	CAG Gln	CTG Leu	AGC Ser	ATG Met	CTG Leu 520	AGA Arg	1587
AAC Asn	AAG Lys	CTG Leu 525	TTC Phe	GGG Gly	CAG Gln	AAC Asn	TGT Cys 530	AGG Arg	ACT Thr	GAG Glu	GAT Asp	CCA Pro	TTA Leu 535	TTG Leu	TCC Ser	1635
TGG Trp	GCT Ala	GAC Asp 540	TTC Phe	ACT Thr	AAG Lys	CGA Arg	GAG Glu 545	AGC Ser	CCT Pro	CCT Pro	GGC Gly	AAG Lys 550	TTA Leu	CCA Pro	TTC Phe	1683
TGG Trp 555	ACA Thr	TGG Trp	CTG Leu	GAC Asp	AAA Lys	ATT Ile 560	CTG Leu	GAG Glu	TTG Leu	GTA Val	CAT His 565	GAC Asp	CAC His	CTG Leu	AAG Lys	1731
GAT Asp 570	CTC Leu	TGG Trp	AAT Asn	GAT Asp	GGA Gly 575	CGC Arg	ATC Ile	ATG Met	GGC Gly	TTT Phe 580	GTG Val	AGT Ser	CGG Arg	AGC Ser	CAG Gln 585	1779
GAG Glu	CGC Arg	CGG Arg	CTG Leu	CTG Leu 590	AAG Lys	AAG Lys	ACC Thr	ATG Met	TCT Ser 595	GGC Gly	ACC Thr	TTT Phe	CTA Leu	CTG Leu 600	CGC Arg	1827
TTC Phe	AGT Ser	GAA Glu 605	TCG Ser	TCA Ser	GAA Glu	GGG Gly	GGC Gly	ATT Ile 610	ACC Thr	TGC Cys	TCC Ser	TGG Trp	GTG Val 615	GAG Glu	CAC His	1875
CAG Gln	GAT Asp 620	GAT Asp	GAC Asp	AAG Lys	GTG Val	CTC Leu	ATC Ile 625	TAC Tyr	TCT Ser	GTG Val	CAA Gln 630	CCG Pro	TAC Tyr	ACG Thr	AAG Lys	1923
GAG Glu 635	GTG Val	CTG Leu	CAG Gln	TCA Ser	CTC Leu	CCG Pro 640	CTG Leu	ACT Thr	GAA Glu	ATC Ile 645	ATC Ile	CGC Arg	CAT His	TAC Tyr	CAG Gln	1971
TTG Leu 650	CTC Leu	ACT Thr	GAG Glu	GAG Glu	AAT Asn 655	ATA Ile	CCT Pro	GAA Glu	AAC Asn	CCA Pro 660	CTG Leu	CGC Arg	TTC Phe	CTC Leu	TAT Tyr 665	2019
CCC Pro	CGA Arg	ATC Ile	CCC Pro	CGG Arg 670	GAT Asp	GAA Glu	GCT Ala	TTT Phe	GGG Gly 675	TGC Cys	TAC Tyr	TAC Tyr	CAG Gln	GAG Glu 680	AAA Lys	2067
GTT Val	AAT Asn	CTC Leu	CAG Gln 685	GAA Glu	CGG Arg	AGG Arg	AAA Lys	TAC Tyr 690	CTG Leu	AAA Lys	CAC His	AGG Arg	CTC Leu 695	ATT Ile	GTG Val	2115
GTC Val	TCT Ser	AAT Asn 700	AGA Arg	CAG Gln	GTG Val	GAT Asp	GAA Glu 705	CTG Leu	CAA Gln	CAA Gln	CCG Pro	CTG Leu 710	GAG Glu	CTT Leu	AAG Lys	2163
CCA Pro 715	GAG Glu	CCA Pro	GAG Glu	CTG Leu	GAG Glu	TCA Ser 720	TTA Leu	GAG Glu	CTG Leu	GAA Glu 725	CTA Leu	GGG Gly	CTG Leu	GTG Val	CCA Pro	2211

GAG CCA GAG CTC AGC CTG GAC TTA GAG CCA CTG CTG AAG GCA GGG CTG Glu Pro Glu Leu Ser Leu Asp Leu Glu Pro Leu Leu Lys Ala Gly Leu 730 735 740 745	2259
GAT CTG GGG CCA GAG CTA GAG TCT GTG CTG GAG TCC ACT CTG GAG CCT Asp Leu Gly Pro Glu Leu Glu Ser Val Leu Glu Ser Thr Leu Glu Pro 750 755 760	2307
GTG ATA GAG CCC ACA CTA TGC ATG GTA TCA CAA ACA GTG CCA GAG CCA Val Ile Glu Pro Thr Leu Cys Met Val Ser Gln Thr Val Pro Glu Pro 765 770 775	2355
GAC CAA GGA CCT GTA TCA CAG CCA GTG CCA GAG CCA GAT TTG CCC TGT Asp Gln Gly Pro Val Ser Gln Pro Val Pro Glu Pro Asp Leu Pro Cys 780 785 790	2403
GAT CTG AGA CAT TTG AAC ACT GAG CCA ATG GAA ATC TTC AGA AAC TGT Asp Leu Arg His Leu Asn Thr Glu Pro Met Glu Ile Phe Arg Asn Cys 795 800 805	2451
GTA AAG ATT GAA GAA ATC ATG CCG AAT GGT GAC CCA CTG TTG GCT GGC Val Lys Ile Glu Glu Ile Met Pro Asn Gly Asp Pro Leu Leu Ala Gly 810 815 820 825	2499
CAG AAC ACC GTG GAT GAG GTT TAC GTC TCC CGC CCC AGC CAC TTC TAC Gln Asn Thr Val Asp Glu Val Tyr Val Ser Arg Pro Ser His Phe Tyr 830 835 840	2547
ACT GAT GGA CCC TTG ATG CCT TCT GAC TTC TAGGAACCAC ATTTCTCTCTG Thr Asp Gly Pro Leu Met Pro Ser Asp Phe 845 850	2597
TTCTTTTTCAT ATCTCTTTGC CCTTCCTACT CCTCATAGCA TGATATTGTT CTCCAAGGAT	2657
GGGAATCAGG CATGTGTCCC TTCCAAGCTG TGTAACTGT TCAAACCTCAG GCCTGTGTGA	2717
CTCCATTGGG GTGAGAGGTG AAAGCATAAC ATGGGTACAG AGGGGACAAC AATGAATCAG	2777
AACAGATGCT GAGCCATAGG TCTAAATAGG ATCCTGGAGG CTGCCTGCTG TGCTGGGAGG	2837
TATAGGGGTC CTGGGGGCAG GCCAGGGCAG TTGACAGGTA CTTGGAGGGC TCAGGGCAGT	2897
GGCTTCTTTC CAGTATGGAA GGATTTC AAC ATTTTAATAG TTGGTTAGGC TAAACTGGTG	2957
CATACTGGCA TTGGCCTTGG TGGGGAGCAC AGACACAGGA TAGGACTCCA TTTCTTTCTT	3017
CCATTCCTTC ATGTCTAGGA TAACTTGCTT TCTTCTTTCC TTTACTCCTG GCTCAAGCCC	3077
TGAATTTCTT CTTTTCCTGC AGGGGTTGAG AGCTTTCTGC CTTAGCCTAC CATGTGAAAC	3137
TCTACCCTGA AGAAAGGGAT GGATAGGAAG TAGACCTCTT TTTCTTACCA GTCTCCTCCC	3197
CTACTCTGCC CCCTAAGCTG GCTGTACCTG TTCCTCCCC ATAAAATGAT CCTGCCAATC	3257
TAAAAA AAA A	3268

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 851 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ala	Gln	Trp	Glu	Met	Leu	Gln	Asn	Leu	Asp	Ser	Pro	Phe	Gln	Asp	1	5	10	15
Gln	Leu	His	Gln	Leu	Tyr	Ser	His	Ser	Leu	Leu	Pro	Val	Asp	Ile	Arg	20	25	30	
Gln	Tyr	Leu	Ala	Val	Trp	Ile	Glu	Asp	Gln	Asn	Trp	Gln	Glu	Ala	Ala	35	40	45	
Leu	Gly	Ser	Asp	Asp	Ser	Lys	Ala	Thr	Met	Leu	Phe	Phe	His	Phe	Leu	50	55	60	
Asp	Gln	Leu	Asn	Tyr	Glu	Cys	Gly	Arg	Cys	Ser	Gln	Asp	Pro	Glu	Ser	65	70	75	80
Leu	Leu	Leu	Gln	His	Asn	Leu	Arg	Lys	Phe	Cys	Arg	Asp	Ile	Gln	Pro	85	90	95	
Phe	Ser	Gln	Asp	Pro	Thr	Gln	Leu	Ala	Glu	Met	Ile	Phe	Asn	Leu	Leu	100	105	110	
Leu	Glu	Glu	Lys	Arg	Ile	Leu	Ile	Gln	Ala	Gln	Arg	Ala	Gln	Leu	Glu	115	120	125	
Gln	Gly	Glu	Pro	Val	Leu	Glu	Thr	Pro	Val	Glu	Ser	Gln	Gln	His	Glu	130	135	140	
Ile	Glu	Ser	Arg	Ile	Leu	Asp	Leu	Arg	Ala	Met	Met	Glu	Lys	Leu	Val	145	150	155	160
Lys	Ser	Ile	Ser	Gln	Leu	Lys	Asp	Gln	Gln	Asp	Val	Phe	Cys	Phe	Arg	165	170	175	
Tyr	Lys	Ile	Gln	Ala	Lys	Gly	Lys	Thr	Pro	Ser	Leu	Asp	Pro	His	Gln	180	185	190	
Thr	Lys	Glu	Gln	Lys	Ile	Leu	Gln	Glu	Thr	Leu	Asn	Glu	Leu	Asp	Lys	195	200	205	
Arg	Arg	Lys	Glu	Val	Leu	Asp	Ala	Ser	Lys	Ala	Leu	Leu	Gly	Arg	Leu	210	215	220	
Thr	Thr	Leu	Ile	Glu	Leu	Leu	Leu	Pro	Lys	Leu	Glu	Glu	Trp	Lys	Ala	225	230	235	240
Gln	Gln	Gln	Lys	Ala	Cys	Ile	Arg	Ala	Pro	Ile	Asp	His	Gly	Leu	Glu	245	250	255	
Gln	Leu	Glu	Thr	Trp	Phe	Thr	Ala	Gly	Ala	Lys	Leu	Leu	Phe	His	Leu	260	265	270	
Arg	Gln	Leu	Leu	Lys	Glu	Leu	Lys	Gly	Leu	Ser	Cys	Leu	Val	Ser	Tyr	275	280	285	
Gln	Asp	Asp	Pro	Leu	Thr	Lys	Gly	Val	Asp	Leu	Arg	Asn	Ala	Gln	Val	290	295	300	
Thr	Glu	Leu	Leu	Gln	Arg	Leu	Leu	His	Arg	Ala	Phe	Val	Val	Glu	Thr	305	310	315	320
Gln	Pro	Cys	Met	Pro	Gln	Thr	Pro	His	Arg	Pro	Leu	Ile	Leu	Lys	Thr	325	330	335	
Gly	Ser	Lys	Phe	Thr	Val	Arg	Thr	Arg	Leu	Leu	Val	Arg	Leu	Gln	Glu	340	345	350	
Gly	Asn	Glu	Ser	Leu	Thr	Val	Glu	Val	Ser	Ile	Asp	Arg	Asn	Pro	Pro	355	360	365	

Gln	Leu	Gln	Gly	Phe	Arg	Lys	Phe	Asn	Ile	Leu	Thr	Ser	Asn	Gln	Lys	370	375	380
Thr	Leu	Thr	Pro	Glu	Lys	Gly	Gln	Ser	Gln	Gly	Leu	Ile	Trp	Asp	Phe	385	390	395
Gly	Tyr	Leu	Thr	Leu	Val	Glu	Gln	Arg	Ser	Gly	Gly	Ser	Gly	Lys	Gly	405	410	415
Ser	Asn	Lys	Gly	Pro	Leu	Gly	Val	Thr	Glu	Glu	Leu	His	Ile	Ile	Ser	420	425	430
Phe	Thr	Val	Lys	Tyr	Thr	Tyr	Gln	Gly	Leu	Lys	Gln	Glu	Leu	Lys	Thr	435	440	445
Asp	Thr	Leu	Pro	Val	Val	Ile	Ile	Ser	Asn	Met	Asn	Gln	Leu	Ser	Ile	450	455	460
Ala	Trp	Ala	Ser	Val	Leu	Trp	Phe	Asn	Leu	Leu	Ser	Pro	Asn	Leu	Gln	465	470	475
Asn	Gln	Gln	Phe	Phe	Ser	Asn	Pro	Pro	Lys	Ala	Pro	Trp	Ser	Leu	Leu	485	490	495
Gly	Pro	Ala	Leu	Ser	Trp	Gln	Phe	Ser	Ser	Tyr	Val	Gly	Arg	Gly	Leu	500	505	510
Asn	Ser	Asp	Gln	Leu	Ser	Met	Leu	Arg	Asn	Lys	Leu	Phe	Gly	Gln	Asn	515	520	525
Cys	Arg	Thr	Glu	Asp	Pro	Leu	Leu	Ser	Trp	Ala	Asp	Phe	Thr	Lys	Arg	530	535	540
Glu	Ser	Pro	Pro	Gly	Lys	Leu	Pro	Phe	Trp	Thr	Trp	Leu	Asp	Lys	Ile	545	550	555
Leu	Glu	Leu	Val	His	Asp	His	Leu	Lys	Asp	Leu	Trp	Asn	Asp	Gly	Arg	565	570	575
Ile	Met	Gly	Phe	Val	Ser	Arg	Ser	Gln	Glu	Arg	Arg	Leu	Leu	Lys	Lys	580	585	590
Thr	Met	Ser	Gly	Thr	Phe	Leu	Leu	Arg	Phe	Ser	Glu	Ser	Ser	Glu	Gly	595	600	605
Gly	Ile	Thr	Cys	Ser	Trp	Val	Glu	His	Gln	Asp	Asp	Asp	Lys	Val	Leu	610	615	620
Ile	Tyr	Ser	Val	Gln	Pro	Tyr	Thr	Lys	Glu	Val	Leu	Gln	Ser	Leu	Pro	625	630	635
Leu	Thr	Glu	Ile	Ile	Arg	His	Tyr	Gln	Leu	Leu	Thr	Glu	Glu	Asn	Ile	645	650	655
Pro	Glu	Asn	Pro	Leu	Arg	Phe	Leu	Tyr	Pro	Arg	Ile	Pro	Arg	Asp	Glu	660	665	670
Ala	Phe	Gly	Cys	Tyr	Tyr	Gln	Glu	Lys	Val	Asn	Leu	Gln	Glu	Arg	Arg	675	680	685
Lys	Tyr	Leu	Lys	His	Arg	Leu	Ile	Val	Val	Ser	Asn	Arg	Gln	Val	Asp	690	695	700
Glu	Leu	Gln	Gln	Pro	Leu	Glu	Leu	Lys	Pro	Glu	Pro	Glu	Leu	Glu	Ser	705	710	715
Leu	Glu	Leu	Glu	Leu	Gly	Leu	Val	Pro	Glu	Pro	Glu	Leu	Ser	Leu	Asp	725	730	735

GAG Glu	CAC His	GCT Ala	GCC Ala	AAT Asn	GAT Asp	GTT Val	TCA Ser	TTT Phe	GCC Ala	ACC Thr	ATC Ile	CGT Arg	TTT Phe	CAT His	GAC Asp	373
	45					50					55					
CTC Leu	CTG Leu	TCA Ser	CAG Gln	CTG Leu	GAT Asp	GAT Asp	CAA Gln	TAT Tyr	AGT Ser	CGC Arg	TTT Phe	TCT Ser	TTG Leu	GAG Glu	AAT Asn	421
60					65					70					75	
AAC Asn	TTC Phe	TTG Leu	CTA Leu	CAG Gln	CAT His	AAC Asn	ATA Ile	AGG Arg	AAA Lys	AGC Ser	AAG Lys	CGT Arg	AAT Asn	CTT Leu	CAG Gln	469
				80					85					90		
GAT Asp	AAT Asn	TTT Phe	CAG Gln	GAA Glu	GAC Asp	CCA Pro	ATC Ile	CAG Gln	ATG Met	TCT Ser	ATG Met	ATC Ile	ATT Ile	TAC Tyr	AGC Ser	517
			95					100					105			
TGT Cys	CTG Leu	AAG Lys	GAA Glu	GAA Glu	AGG Arg	AAA Lys	ATT Ile	CTG Leu	GAA Glu	AAC Asn	GCC Ala	CAG Gln	AGA Arg	TTT Phe	AAT Asn	565
		110					115					120				
CAG Gln	GCT Ala	CAG Gln	TCG Ser	GGG Gly	AAT Asn	ATT Ile	CAG Gln	AGC Ser	ACA Thr	GTG Val	ATG Met	TTA Leu	GAC Asp	AAA Lys	CAG Gln	613
	125					130					135					
AAA Lys	GAG Glu	CTT Leu	GAC Asp	AGT Ser	AAA Lys	GTC Val	AGA Arg	AAT Asn	GTG Val	AAG Lys	GAC Asp	AAG Lys	GTT Val	ATG Met	TGT Cys	661
140					145					150					155	
ATA Ile	GAG Glu	CAT His	GAA Glu	ATC Ile	AAG Lys	AGC Ser	CTG Leu	GAA Glu	GAT Asp	TTA Leu	CAA Gln	GAT Asp	GAA Glu	TAT Tyr	GAC Asp	709
				160					165					170		
TTC Phe	AAA Lys	TGC Cys	AAA Lys	ACC Thr	TTG Leu	CAG Gln	AAC Asn	AGA Arg	GAA Glu	CAC His	GAG Glu	ACC Thr	AAT Asn	GGT Gly	GTG Val	757
			175					180					185			
GCA Ala	AAG Lys	AGT Ser	GAT Asp	CAG Gln	AAA Lys	CAA Gln	GAA Glu	CAG Gln	CTG Leu	TTA Leu	CTC Leu	AAG Lys	AAG Lys	ATG Met	TAT Tyr	805
		190				195						200				
TTA Leu	ATG Met	CTT Leu	GAC Asp	AAT Asn	AAG Lys	AGA Arg	AAG Lys	GAA Glu	GTA Val	GTT Val	CAC His	AAA Lys	ATA Ile	ATA Ile	GAG Glu	853
	205					210					215					
TTG Leu	CTG Leu	AAT Asn	GTC Val	ACT Thr	GAA Glu	CTT Leu	ACC Thr	CAG Gln	AAT Asn	GCC Ala	CTG Leu	ATT Ile	AAT Asn	GAT Asp	GAA Glu	901
220					225					230					235	
CTA Leu	GTG Val	GAG Glu	TGG Trp	AAG Lys	CGG Arg	AGA Arg	CAG Gln	CAG Gln	AGC Ser	GCC Ala	TGT Cys	ATT Ile	GGG Gly	GGG Gly	CCG Pro	949
				240					245				250			
CCC Pro	AAT Asn	GCT Ala	TGC Cys	TTG Leu	GAT Asp	CAG Gln	CTG Leu	CAG Gln	AAC Asn	TGG Trp	TTC Phe	ACT Thr	ATA Ile	GTT Val	GCG Ala	997
			255				260						265			
GAG Glu	AGT Ser	CTG Leu	CAG Gln	CAA Gln	GTT Val	CGG Arg	CAG Gln	CAG Gln	CTT Leu	AAA Lys	AAG Lys	TTG Leu	GAG Glu	GAA Glu	TTG Leu	1045
		270					275					280				
GAA Glu	CAG Gln	AAA Lys	TAC Tyr	ACC Thr	TAC Tyr	GAA Glu	CAT His	GAC Asp	CCT Pro	ATC Ile	ACA Thr	AAA Lys	AAC Asn	AAA Lys	CAA Gln	1093
	285					290					295					
GTG Val	TTA Leu	TGG Trp	GAC Asp	CGC Arg	ACC Thr	TTC Phe	AGT Ser	CTT Leu	TTC Phe	CAG Gln	CAG Gln	CTC Leu	ATT Ile	CAG Gln	AGC Ser	1141
300					305					310					315	

TCG	TTT	GTG	GTG	GAA	AGA	CAG	CCC	TGC	ATG	CCA	ACG	CAC	CCT	CAG	AGG	1189
Ser	Phe	Val	Val	Glu	Arg	Gln	Pro	Cys	Met	Pro	Thr	His	Pro	Gln	Arg	
				320					325					330		
CCG	CTG	GTC	TTG	AAG	ACA	GGG	GTC	CAG	TTC	ACT	GTG	AAG	TTG	AGA	CTG	1237
Pro	Leu	Val	Leu	Lys	Thr	Gly	Val	Gln	Phe	Thr	Val	Lys	Leu	Arg	Leu	
			335					340					345			
TTG	GTG	AAA	TTG	CAA	GAG	CTG	AAT	TAT	AAT	TTG	AAA	GTC	AAA	GTC	TTA	1285
Leu	Val	Lys	Leu	Gln	Glu	Leu	Asn	Tyr	Asn	Leu	Lys	Val	Lys	Val	Leu	
		350					355					360				
TTT	GAT	AAA	GAT	GTG	AAT	GAG	AGA	AAT	ACA	GTA	AAA	GGA	TTT	AGG	AAG	1333
Phe	Asp	Lys	Asp	Val	Asn	Glu	Arg	Asn	Thr	Val	Lys	Gly	Phe	Arg	Lys	
	365					370					375					
TTC	AAC	ATT	TTG	GGC	ACG	CAC	ACA	AAA	GTG	ATG	AAC	ATG	GAG	GAG	TCC	1381
Phe	Asn	Ile	Leu	Gly	Thr	His	Thr	Lys	Val	Met	Asn	Met	Glu	Glu	Ser	
					385					390					395	
ACC	AAT	GGC	AGT	CTG	GCG	GCT	GAA	TTT	CGG	CAC	CTG	CAA	TTG	AAA	GAA	1429
Thr	Asn	Gly	Ser	Leu	Ala	Ala	Glu	Phe	Arg	His	Leu	Gln	Leu	Lys	Glu	
				400					405					410		
CAG	AAA	AAT	GCT	GGC	ACC	AGA	ACG	AAT	GAG	GGT	CCT	CTC	ATC	GTT	ACT	1477
Gln	Lys	Asn	Ala	Gly	Thr	Arg	Thr	Asn	Glu	Gly	Pro	Leu	Ile	Val	Thr	
			415					420					425			
GAA	GAG	CTT	CAC	TCC	CTT	AGT	TTT	GAA	ACC	CAA	TTG	TGC	CAG	CCT	GGT	1525
Glu	Glu	Leu	His	Ser	Leu	Ser	Phe	Glu	Thr	Gln	Leu	Cys	Gln	Pro	Gly	
		430					435					440				
TTG	GTA	ATT	GAC	CTC	GAG	ACG	ACC	TCT	CTG	CCC	GTT	GTG	GTG	ATC	TCC	1573
Leu	Val	Ile	Asp	Leu	Glu	Thr	Thr	Ser	Leu	Pro	Val	Val	Val	Ile	Ser	
	445					450					455					
AAC	GTC	AGC	CAG	CTC	CCG	AGC	GGT	TGG	GCC	TCC	ATC	CTT	TGG	TAC	AAC	1621
Asn	Val	Ser	Gln	Leu	Pro	Ser	Gly	Trp	Ala	Ser	Ile	Leu	Trp	Tyr	Asn	
	460				465					470					475	
ATG	CTG	GTG	GCG	GAA	CCC	AGG	AAT	CTG	TCC	TTC	TTC	CTG	ACT	CCA	CCA	1669
Met	Leu	Val	Ala	Glu	Pro	Arg	Asn	Leu	Ser	Phe	Phe	Leu	Thr	Pro	Pro	
			480					485						490		
TGT	GCA	CGA	TGG	GCT	CAG	CTT	TCA	GAA	GTG	CTG	AGT	TGG	CAG	TTT	TCT	1717
Cys	Ala	Arg	Trp	Ala	Gln	Leu	Ser	Glu	Val	Leu	Ser	Trp	Gln	Phe	Ser	
			495					500					505			
TCT	GTC	ACC	AAA	AGA	GGT	CTC	AAT	GTG	GAC	CAG	CTG	AAC	ATG	TTG	GGA	1765
Ser	Val	Thr	Lys	Arg	Gly	Leu	Asn	Val	Asp	Gln	Leu	Asn	Met	Leu	Gly	
		510					515					520				
GAG	AAG	CTT	CTT	GGT	CCT	AAC	GCC	AGC	CCC	GAT	GGT	CTC	ATT	CCG	TGG	1813
Glu	Lys	Leu	Leu	Gly	Pro	Asn	Ala	Ser	Pro	Asp	Gly	Leu	Ile	Pro	Trp	
	525					530				535						
ACG	AGG	TTT	TGT	AAG	GAA	AAT	ATA	AAT	GAT	AAA	AAT	TTT	CCC	TTC	TGG	1861
Thr	Arg	Phe	Cys	Lys	Glu	Asn	Ile	Asn	Asp	Lys	Asn	Phe	Pro	Phe	Trp	
	540				545				550						555	
CTT	TGG	ATT	GAA	AGC	ATC	CTA	GAA	CTC	ATT	AAA	AAA	CAC	CTG	CTC	CCT	1909
Leu	Trp	Ile	Glu	Ser	Ile	Leu	Glu	Leu	Ile	Lys	Lys	His	Leu	Leu	Pro	
			560					565						570		
CTC	TGG	AAT	GAT	GGG	TGC	ATC	ATG	GGC	TTC	ATC	AGC	AAG	GAG	CGA	GAG	1957
Leu	Trp	Asn	Asp	Gly	Cys	Ile	Met	Gly	Phe	Ile	Ser	Lys	Glu	Arg	Glu	
			575					580					585			

CGT GCC CTG TTG AAG GAC CAG CAG CCG GGG ACC TTC CTG CTG CGG TTC	2005
Arg Ala Leu Leu Lys Asp Gln Gln Pro Gly Thr Phe Leu Leu Arg Phe	
590 595 600	
AGT GAG AGC TCC CGG GAA GGG GCC ATC ACA TTC ACA TGG GTG GAG CGG	2053
Ser Glu Ser Ser Arg Glu Gly Ala Ile Thr Phe Thr Trp Val Glu Arg	
605 610 615	
TCC CAG AAC GGA GGC GAA CCT GAC TTC CAT GCG GTT GAA CCC TAC ACG	2101
Ser Gln Asn Gly Gly Glu Pro Asp Phe His Ala Val Glu Pro Tyr Thr	
620 625 630 635	
AAG AAA GAA CTT TCT GCT GTT ACT TTC CCT GAC ATC ATT CGC AAT TAC	2149
Lys Lys Glu Leu Ser Ala Val Thr Phe Pro Asp Ile Ile Arg Asn Tyr	
640 645 650	
AAA GTC ATG GCT GCT GAG AAT ATT CCT GAG AAT CCC CTG AAG TAT CTG	2197
Lys Val Met Ala Ala Glu Asn Ile Pro Glu Asn Pro Leu Lys Tyr Leu	
655 660 665	
TAT CCA AAT ATT GAC AAA GAC CAT GCC TTT GGA AAG TAT TAC TCC AGG	2245
Tyr Pro Asn Ile Asp Lys Asp His Ala Phe Gly Lys Tyr Tyr Ser Arg	
670 675 680	
CCA AAG GAA GCA CCA GAG CCA ATG GAA CTT GAT GGC CCT AAA GGA ACT	2293
Pro Lys Glu Ala Pro Glu Pro Met Glu Leu Asp Gly Pro Lys Gly Thr	
685 690 695	
GGA TAT ATC AAG ACT GAG TTG ATT TCT GTG TCT GAA GTT CAC CCT TCT	2341
Gly Tyr Ile Lys Thr Glu Leu Ile Ser Val Ser Glu Val His Pro Ser	
700 705 710 715	
AGA CTT CAG ACC ACA GAC AAC CTG CTC CCC ATG TCT CCT GAG GAG TTT	2389
Arg Leu Gln Thr Thr Asp Asn Leu Leu Pro Met Ser Pro Glu Glu Phe	
720 725 730	
GAC GAG GTG TCT CGG ATA GTG GGC TCT GTA GAA TTC GAC AGT ATG ATG	2437
Asp Glu Val Ser Arg Ile Val Gly Ser Val Glu Phe Asp Ser Met Met	
735 740 745	
AAC ACA GTA TAGAGCATGA ATTTTTTTTCA TCTTCTCTGG CGACAGTTTT	2486
Asn Thr Val	
750	
CCTTCTCATC TGTGATTCCC TCCTGCTACT CTGTTCCCTC ACATCCTGTG TTTCTAGGGA	2546
AATGAAAGAA AGGCCAGCAA ATTCGCTGCA ACCTGTTGAT AGCAAGTGAA TTTTCTCTCTA	2606
ACTCAGAAAC ATCAGTTACT CTGAAGGGCA TCATGCATCT TACTGAAGGT AAAATTGAAA	2666
GGCATTCTCT GAAGAGTGGG TTTCACAAGT GAAAAACATC CAGATACACC CAAAGTATCA	2726
GGACGAGAAT GAGGGTCCTT TGGGAAAGGA GAAGTTAAGC AACATCTAGC AAATGTTATG	2786
CATAAAGTCA GTGCCCAACT GTTATAGGTT GTTGGATAAA TCAGTGGTTA TTTAGGGAAC	2846
TGCTTGACGT AGGAACGGTA AATTTCTGTG GGAGAATTCT TACATGTTTT CTTTGCTTTA	2906
AGTGTAAGTG GCAGTTTTCC ATTGGTTTAC CTGTGAAATA GTTCAAAGCC AAGTTTATAT	2966
ACAATTATAT CAGTCCTCTT TCAAAGGTAG CCATCATGGA TCTGGTAGGG GGAAAATGTG	3026
TATTTTATTA CATCTTTCAC ATTGGCTATT TAAAGACAAA GACAAATTCT GTTTCTTGAG	3086
AAGAGAACAT TTCCAAATTC ACAAGTTGTG TTTGATATCC AAAGCTGAAT ACATTCTGCT	3146
TTCATCTTGG TCACATACAA TTATTTTAC AGTTCTCCCA AGGGAGTTAG GCTATTACAA	3206
ACCACTCATT CAAAAGTTGA AATTAACCAT AGATGTAGAT AAACCTCAGAA ATTTAATTCA	3266

TGTTCCTTAA ATGGGCTACT TTGTCCTTTT TGTATTAGG GTGGTATTTA GTCTATTAGC 3326
 CACAAAATTG GGAAAGGAGT AGAAAAAGCA GTAAGTACATA ACTTGAATAA TACACCAGAG 3386
 ATAATATGAG AATCAGATCA TTTCAAACT CATTTCCTAT GTAAGTGCAT TGAGAACTGC 3446
 ATATGTTTCG CTGATATATG TGTTTTTCAC ATTTGCGAAT GGTTCATTTC TCTCTCCTGT 3506
 ACTTTTTCCA GACACTTTTT TGAGTGGATG ATGTTTCGTG AAGTATACTG TATTTTTACC 3566
 TTTTTCCTTC CTTATCACTG ACACAAAAAG TAGATTAAGA GATGGGTTTG ACAAGGTTCT 3626
 TCCCTTTTAC ATACTGCTGT CTATGTGGCT GTATCTTGTT TTTCCACTAC TGCTACCACA 3686
 ACTATATTAT CATGCAAATG CTGTATTCTT CTTTGGTGGA GATAAAGATT TCTTGAGTTT 3746
 TGTTTTAAAA TTAAAGCTAA AGTATCTGTA TTGCATTAAA TATAATATCG ACACAGTGCT 3806
 TTCCGTGGCA CTGCATACAA TCTGAGGCCT CCTCTCTCAG TTTTATATA GATGGCGAGA 3866
 ACCTAAGTTT CAGTTGATTT TACAATTGAA ATGACTAAAA AACAAAGAAG ACAACATTAA 3926
 AAACAATATT GTTTCTA 3943

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 750 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ser Gln Trp Tyr Glu Leu Gln Gln Leu Asp Ser Lys Phe Leu Glu
 1 5 10 15
 Gln Val His Gln Leu Tyr Asp Asp Ser Phe Pro Met Glu Ile Arg Gln
 20 25 30
 Tyr Leu Ala Gln Trp Leu Glu Lys Gln Asp Trp Glu His Ala Ala Asn
 35 40 45
 Asp Val Ser Phe Ala Thr Ile Arg Phe His Asp Leu Leu Ser Gln Leu
 50 55 60
 Asp Asp Gln Tyr Ser Arg Phe Ser Leu Glu Asn Asn Phe Leu Leu Gln
 65 70 75 80
 His Asn Ile Arg Lys Ser Lys Arg Asn Leu Gln Asp Asn Phe Gln Glu
 85 90 95
 Asp Pro Ile Gln Met Ser Met Ile Ile Tyr Ser Cys Leu Lys Glu Glu
 100 105 110
 Arg Lys Ile Leu Glu Asn Ala Gln Arg Phe Asn Gln Ala Gln Ser Gly
 115 120 125
 Asn Ile Gln Ser Thr Val Met Leu Asp Lys Gln Lys Glu Leu Asp Ser
 130 135 140
 Lys Val Arg Asn Val Lys Asp Lys Val Met Cys Ile Glu His Glu Ile
 145 150 155 160
 Lys Ser Leu Glu Asp Leu Gln Asp Glu Tyr Asp Phe Lys Cys Lys Thr
 165 170 175

Leu	Gln	Asn	Arg	Glu	His	Glu	Thr	Asn	Gly	Val	Ala	Lys	Ser	Asp	Gln	180	185	190
Lys	Gln	Glu	Gln	Leu	Leu	Leu	Lys	Lys	Met	Tyr	Leu	Met	Leu	Asp	Asn	195	200	205
Lys	Arg	Lys	Glu	Val	Val	His	Lys	Ile	Ile	Glu	Leu	Leu	Asn	Val	Thr	210	215	220
Glu	Leu	Thr	Gln	Asn	Ala	Leu	Ile	Asn	Asp	Glu	Leu	Val	Glu	Trp	Lys	225	230	235
Arg	Arg	Gln	Gln	Ser	Ala	Cys	Ile	Gly	Gly	Pro	Pro	Asn	Ala	Cys	Leu	245	250	255
Asp	Gln	Leu	Gln	Asn	Trp	Phe	Thr	Ile	Val	Ala	Glu	Ser	Leu	Gln	Gln	260	265	270
Val	Arg	Gln	Gln	Leu	Lys	Lys	Leu	Glu	Glu	Leu	Glu	Gln	Lys	Tyr	Thr	275	280	285
Tyr	Glu	His	Asp	Pro	Ile	Thr	Lys	Asn	Lys	Gln	Val	Leu	Trp	Asp	Arg	290	295	300
Thr	Phe	Ser	Leu	Phe	Gln	Gln	Leu	Ile	Gln	Ser	Ser	Phe	Val	Val	Glu	305	310	315
Arg	Gln	Pro	Cys	Met	Pro	Thr	His	Pro	Gln	Arg	Pro	Leu	Val	Leu	Lys	325	330	335
Thr	Gly	Val	Gln	Phe	Thr	Val	Lys	Leu	Arg	Leu	Leu	Val	Lys	Leu	Gln	340	345	350
Glu	Leu	Asn	Tyr	Asn	Leu	Lys	Val	Lys	Val	Leu	Phe	Asp	Lys	Asp	Val	355	360	365
Asn	Glu	Arg	Asn	Thr	Val	Lys	Gly	Phe	Arg	Lys	Phe	Asn	Ile	Leu	Gly	370	375	380
Thr	His	Thr	Lys	Val	Met	Asn	Met	Glu	Glu	Ser	Thr	Asn	Gly	Ser	Leu	385	390	395
Ala	Ala	Glu	Phe	Arg	His	Leu	Gln	Leu	Lys	Glu	Gln	Lys	Asn	Ala	Gly	405	410	415
Thr	Arg	Thr	Asn	Glu	Gly	Pro	Leu	Ile	Val	Thr	Glu	Glu	Leu	His	Ser	420	425	430
Leu	Ser	Phe	Glu	Thr	Gln	Leu	Cys	Gln	Pro	Gly	Leu	Val	Ile	Asp	Leu	435	440	445
Glu	Thr	Thr	Ser	Leu	Pro	Val	Val	Val	Ile	Ser	Asn	Val	Ser	Gln	Leu	450	455	460
Pro	Ser	Gly	Trp	Ala	Ser	Ile	Leu	Trp	Tyr	Asn	Met	Leu	Val	Ala	Glu	465	470	475
Pro	Arg	Asn	Leu	Ser	Phe	Phe	Leu	Thr	Pro	Pro	Cys	Ala	Arg	Trp	Ala	485	490	495
Gln	Leu	Ser	Glu	Val	Leu	Ser	Trp	Gln	Phe	Ser	Ser	Val	Thr	Lys	Arg	500	505	510
Gly	Leu	Asn	Val	Asp	Gln	Leu	Asn	Met	Leu	Gly	Glu	Lys	Leu	Leu	Gly	515	520	525
Pro	Asn	Ala	Ser	Pro	Asp	Gly	Leu	Ile	Pro	Trp	Thr	Arg	Phe	Cys	Lys	530	535	540

Glu Asn Ile Asn Asp Lys Asn Phe Pro Phe Trp Leu Trp Ile Glu Ser
 545 550 555 560
 Ile Leu Glu Leu Ile Lys Lys His Leu Leu Pro Leu Trp Asn Asp Gly
 565 570 575
 Cys Ile Met Gly Phe Ile Ser Lys Glu Arg Glu Arg Ala Leu Leu Lys
 580 585 590
 Asp Gln Gln Pro Gly Thr Phe Leu Leu Arg Phe Ser Glu Ser Ser Arg
 595 600 605
 Glu Gly Ala Ile Thr Phe Thr Trp Val Glu Arg Ser Gln Asn Gly Gly
 610 615 620
 Glu Pro Asp Phe His Ala Val Glu Pro Tyr Thr Lys Lys Glu Leu Ser
 625 630 635 640
 Ala Val Thr Phe Pro Asp Ile Ile Arg Asn Tyr Lys Val Met Ala Ala
 645 650 655
 Glu Asn Ile Pro Glu Asn Pro Leu Lys Tyr Leu Tyr Pro Asn Ile Asp
 660 665 670
 Lys Asp His Ala Phe Gly Lys Tyr Tyr Ser Arg Pro Lys Glu Ala Pro
 675 680 685
 Glu Pro Met Glu Leu Asp Gly Pro Lys Gly Thr Gly Tyr Ile Lys Thr
 690 695 700
 Glu Leu Ile Ser Val Ser Glu Val His Pro Ser Arg Leu Gln Thr Thr
 705 710 715 720
 Asp Asn Leu Leu Pro Met Ser Pro Glu Glu Phe Asp Glu Val Ser Arg
 725 730 735
 Ile Val Gly Ser Val Glu Phe Asp Ser Met Met Asn Thr Val
 740 745 750

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2607 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 197..2335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATTAAACCTC TCGCCGAGCC CCTCCGAGCA CTCTGCGCCG GAAAGTTTCA TTTGCTGTAT	60
GCCATCCTCG AGAGCTGTCT AGGTAAACGT TCGCACTCTG TGTATATAAC CTCGACAGTC	120
TTGGCACCTA ACGTGCTGTG CGTAGCTGCT CCTTTGGTTG AATCCCCAGG CCCTTGTTGG	180

GGCACAAAGGT GGCAGG ATG TCT CAG TGG TAC GAA CTT CAG CAG CTT GAC	229
Met Ser Gln Trp Tyr Glu Leu Gln Gln Leu Asp	
1 5 10	
TCA AAA TTC CTG GAG CAG GTT CAC CAG CTT TAT GAT GAC AGT TTT CCC	277
Ser Lys Phe Leu Glu Gln Val His Gln Leu Tyr Asp Asp Ser Phe Pro	
15 20 25	
ATG GAA ATC AGA CAG TAC CTG GCA CAG TGG TTA GAA AAG CAA GAC TGG	325
Met Glu Ile Arg Gln Tyr Leu Ala Gln Trp Leu Glu Lys Gln Asp Trp	
30 35 40	
GAG CAC GCT GCC AAT GAT GTT TCA TTT GCC ACC ATC CGT TTT CAT GAC	373
Glu His Ala Ala Asn Asp Val Ser Phe Ala Thr Ile Arg Phe His Asp	
45 50 55	
CTC CTG TCA CAG CTG GAT GAT CAA TAT AGT CGC TTT TCT TTG GAG AAT	421
Leu Leu Ser Gln Leu Asp Asp Gln Tyr Ser Arg Phe Ser Leu Glu Asn	
60 65 70 75	
AAC TTC TTG CTA CAG CAT AAC ATA AGG AAA AGC AAG CGT AAT CTT CAG	469
Asn Phe Leu Leu Gln His Asn Ile Arg Lys Ser Lys Arg Asn Leu Gln	
80 85 90	
GAT AAT TTT CAG GAA GAC CCA ATC CAG ATG TCT ATG ATC ATT TAC AGC	517
Asp Asn Phe Gln Glu Asp Pro Ile Gln Met Ser Met Ile Ile Tyr Ser	
95 100 105	
TGT CTG AAG GAA GAA AGG AAA ATT CTG GAA AAC GCC CAG AGA TTT AAT	565
Cys Leu Lys Glu Glu Arg Lys Ile Leu Glu Asn Ala Gln Arg Phe Asn	
110 115 120	
CAG GCT CAG TCG GGG AAT ATT CAG AGC ACA GTG ATG TTA GAC AAA CAG	613
Gln Ala Gln Ser Gly Asn Ile Gln Ser Thr Val Met Leu Asp Lys Gln	
125 130 135	
AAA GAG CTT GAC AGT AAA GTC AGA AAT GTG AAG GAC AAG GTT ATG TGT	661
Lys Glu Leu Asp Ser Lys Val Arg Asn Val Lys Asp Lys Val Met Cys	
140 145 150 155	
ATA GAG CAT GAA ATC AAG AGC CTG GAA GAT TTA CAA GAT GAA TAT GAC	709
Ile Glu His Glu Ile Lys Ser Leu Glu Asp Leu Gln Asp Glu Tyr Asp	
160 165 170	
TTC AAA TGC AAA ACC TTG CAG AAC AGA GAA CAC GAG ACC AAT GGT GTG	757
Phe Lys Cys Lys Thr Leu Gln Asn Arg Glu His Glu Thr Asn Gly Val	
175 180 185	
GCA AAG AGT GAT CAG AAA CAA GAA CAG CTG TTA CTC AAG AAG ATG TAT	805
Ala Lys Ser Asp Gln Lys Gln Glu Gln Leu Leu Leu Lys Lys Met Tyr	
190 195 200	
TTA ATG CTT GAC AAT AAG AGA AAG GAA GTA GTT CAC AAA ATA ATA GAG	853
Leu Met Leu Asp Asn Lys Arg Lys Glu Val Val His Lys Ile Ile Glu	
205 210 215	
TTG CTG AAT GTC ACT GAA CTT ACC CAG AAT GCC CTG ATT AAT GAT GAA	901
Leu Leu Asn Val Thr Glu Leu Thr Gln Asn Ala Leu Ile Asn Asp Glu	
220 225 230 235	
CTA GTG GAG TGG AAG CGG AGA CAG CAG AGC GCC TGT ATT GGG GGG CCG	949
Leu Val Glu Trp Lys Arg Arg Gln Gln Ser Ala Cys Ile Gly Gly Pro	
240 245 250	
CCC AAT GCT TGC TTG GAT CAG CTG CAG AAC TGG TTC ACT ATA GTT GCG	997
Pro Asn Ala Cys Leu Asp Gln Leu Gln Asn Trp Phe Thr Ile Val Ala	
255 260 265	
GAG AGT CTG CAG CAA GTT CGG CAG CAG CTT AAA AAG TTG GAG GAA TTG	1045

Glu	Ser	Leu	Gln	Gln	Val	Arg	Gln	Gln	Leu	Lys	Lys	Leu	Glu	Glu	Leu	
		270					275					280				
GAA	CAG	AAA	TAC	ACC	TAC	GAA	CAT	GAC	CCT	ATC	ACA	AAA	AAC	AAA	CAA	1093
Glu	Gln	Lys	Tyr	Thr	Tyr	Glu	His	Asp	Pro	Ile	Thr	Lys	Asn	Lys	Gln	
	285					290					295					
GTG	TTA	TGG	GAC	CGC	ACC	TTC	AGT	CTT	TTC	CAG	CAG	CTC	ATT	CAG	AGC	1141
Val	Leu	Trp	Asp	Arg	Thr	Phe	Ser	Leu	Phe	Gln	Gln	Leu	Ile	Gln	Ser	
300					305					310					315	
TCG	TTT	GTG	GTG	GAA	AGA	CAG	CCC	TGC	ATG	CCA	ACG	CAC	CCT	CAG	AGG	1189
Ser	Phe	Val	Val	Glu	Arg	Gln	Pro	Cys	Met	Pro	Thr	His	Pro	Gln	Arg	
				320					325					330		
CCG	CTG	GTC	TTG	AAG	ACA	GGG	GTC	CAG	TTC	ACT	GTG	AAG	TTG	AGA	CTG	1237
Pro	Leu	Val	Leu	Lys	Thr	Gly	Val	Gln	Phe	Thr	Val	Lys	Leu	Arg	Leu	
			335					340					345			
TTG	GTG	AAA	TTG	CAA	GAG	CTG	AAT	TAT	AAT	TTG	AAA	GTC	AAA	GTC	TTA	1285
Leu	Val	Lys	Leu	Gln	Glu	Leu	Asn	Tyr	Asn	Leu	Lys	Val	Lys	Val	Leu	
		350					355					360				
TTT	GAT	AAA	GAT	GTG	AAT	GAG	AGA	AAT	ACA	GTA	AAA	GGA	TTT	AGG	AAG	1333
Phe	Asp	Lys	Asp	Val	Asn	Glu	Arg	Asn	Thr	Val	Lys	Gly	Phe	Arg	Lys	
	365					370					375					
TTC	AAC	ATT	TTG	GGC	ACG	CAC	ACA	AAA	GTG	ATG	AAC	ATG	GAG	GAG	TCC	1381
Phe	Asn	Ile	Leu	Gly	Thr	His	Thr	Lys	Val	Met	Asn	Met	Glu	Glu	Ser	
380					385					390					395	
ACC	AAT	GGC	AGT	CTG	GCG	GCT	GAA	TTT	CGG	CAC	CTG	CAA	TTG	AAA	GAA	1429
Thr	Asn	Gly	Ser	Leu	Ala	Ala	Glu	Phe	Arg	His	Leu	Gln	Leu	Lys	Glu	
				400					405					410		
CAG	AAA	AAT	GCT	GGC	ACC	AGA	ACG	AAT	GAG	GGT	CCT	CTC	ATC	GTT	ACT	1477
Gln	Lys	Asn	Ala	Gly	Thr	Arg	Thr	Asn	Glu	Gly	Pro	Leu	Ile	Val	Thr	
			415					420					425			
GAA	GAG	CTT	CAC	TCC	CTT	AGT	TTT	GAA	ACC	CAA	TTG	TGC	CAG	CCT	GGT	1525
Glu	Glu	Leu	His	Ser	Leu	Ser	Phe	Glu	Thr	Gln	Leu	Cys	Gln	Pro	Gly	
		430					435					440				
TTG	GTA	ATT	GAC	CTC	GAG	ACG	ACC	TCT	CTG	CCC	GTT	GTG	GTG	ATC	TCC	1573
Leu	Val	Ile	Asp	Leu	Glu	Thr	Thr	Ser	Leu	Pro	Val	Val	Val	Ile	Ser	
	445					450					455					
AAC	GTC	AGC	CAG	CTC	CCG	AGC	GGT	TGG	GCC	TCC	ATC	CTT	TGG	TAC	AAC	1621
Asn	Val	Ser	Gln	Leu	Pro	Ser	Gly	Trp	Ala	Ser	Ile	Leu	Trp	Tyr	Asn	
460					465					470					475	
ATG	CTG	GTG	GCG	GAA	CCC	AGG	AAT	CTG	TCC	TTC	TTC	CTG	ACT	CCA	CCA	1669
Met	Leu	Val	Ala	Glu	Pro	Arg	Asn	Leu	Ser	Phe	Phe	Leu	Thr	Pro	Pro	
				480				485						490		
TGT	GCA	CGA	TGG	GCT	CAG	CTT	TCA	GAA	GTG	CTG	AGT	TGG	CAG	TTT	TCT	1717
Cys	Ala	Arg	Trp	Ala	Gln	Leu	Ser	Glu	Val	Leu	Ser	Trp	Gln	Phe	Ser	
			495					500					505			
TCT	GTC	ACC	AAA	AGA	GGT	CTC	AAT	GTG	GAC	CAG	CTG	AAC	ATG	TTG	GGA	1765
Ser	Val	Thr	Lys	Arg	Gly	Leu	Asn	Val	Asp	Gln	Leu	Asn	Met	Leu	Gly	
		510					515					520				
GAG	AAG	CTT	CTT	GGT	CCT	AAC	GCC	AGC	CCC	GAT	GGT	CTC	ATT	CCG	TGG	1813
Glu	Lys	Leu	Leu	Gly	Pro	Asn	Ala	Ser	Pro	Asp	Gly	Leu	Ile	Pro	Trp	
	525					530					535					

ACG Thr 540	AGG Arg	TTT Phe	TGT Cys	AAG Lys	GAA Glu 545	AAT Asn	ATA Ile	AAT Asn	GAT Asp	AAA Lys 550	AAT Asn	TTT Phe	CCC Pro	TTC Phe	TGG Trp 555	1861
CTT Leu	TGG Trp	ATT Ile	GAA Glu	AGC Ser 560	ATC Ile	CTA Leu	GAA Glu	CTC Leu	ATT Ile 565	AAA Lys	AAA Lys	CAC His	CTG Leu	CTC Leu 570	CCT Pro	1909
CTC Leu	TGG Trp	AAT Asn	GAT Asp 575	GGG Gly	TGC Cys	ATC Ile	ATG Met	GGC Gly 580	TTC Phe	ATC Ile	AGC Ser	AAG Lys	GAG Glu 585	CGA Arg	GAG Glu	1957
CGT Arg	GCC Ala	CTG Leu 590	TTG Leu	AAG Lys	GAC Asp	CAG Gln	CAG Gln 595	CCG Pro	GGG Gly	ACC Thr	TTC Phe	CTG Leu 600	CTG Leu	CGG Arg	TTC Phe	2005
AGT Ser 605	GAG Glu	AGC Ser	TCC Ser	CGG Arg	GAA Glu	GGG Gly 610	GCC Ala	ATC Ile	ACA Thr	TTC Phe	ACA Thr 615	TGG Trp	GTG Val	GAG Glu	CGG Arg	2053
TCC Ser 620	CAG Gln	AAC Asn	GGA Gly	GGC Gly	GAA Glu 625	CCT Pro	GAC Asp	TTC Phe	CAT His	GCG Ala 630	GTT Val	GAA Glu	CCC Pro	TAC Tyr	ACG Thr 635	2101
AAG Lys	AAA Lys	GAA Glu	CTT Leu	TCT Ser 640	GCT Ala	GTT Val	ACT Thr	TTC Phe	CCT Pro 645	GAC Asp	ATC Ile	ATT Ile	CGC Arg	AAT Asn 650	TAC Tyr	2149
AAA Lys	GTC Val	ATG Met	GCT Ala 655	GCT Ala	GAG Glu	AAT Asn	ATT Ile	CCT Pro 660	GAG Glu	AAT Asn	CCC Pro	CTG Leu	AAG Lys 665	TAT Tyr	CTG Leu	2197
TAT Tyr	CCA Pro	AAT Asn 670	ATT Ile	GAC Asp	AAA Lys	GAC Asp	CAT His 675	GCC Ala	TTT Phe	GGA Gly	AAG Lys	TAT Tyr 680	TAC Tyr	TCC Ser	AGG Arg	2245
CCA Pro 685	AAG Lys	GAA Glu	GCA Ala	CCA Pro	GAG Glu	CCA Pro 690	ATG Met	GAA Glu	CTT Leu	GAT Asp	GGC Gly 695	CCT Pro	AAA Lys	GGA Gly	ACT Thr	2293
GGA Gly 700	TAT Tyr	ATC Ile	AAG Lys	ACT Thr	GAG Glu 705	TTG Leu	ATT Ile	TCT Ser	GTG Val	TCT Ser 710	GAA Glu	GTG Val	TAAGTGAACA			2342
CAGAAGAGTG	ACATGTTTAC	AAACCTCAAG	CCAGCCTTGC	TCCTGGCTGG	GGCCTGTTGA											2402
AGATGCTTGT	ATTTTACTTT	TCCATTGTAA	TTGCTATCGC	CATCACAGCT	GAAGTTGTTG											2462
AGATCCCCGT	GTTACTGCCT	ATCAGCATTT	TACTACTTTA	AAAAAAAAAA	AAAAAGCCAA											2522
AAACCAAATT	TGTATTTAAG	GTATATAAAT	TTTCCCAAAA	CTGATACCCT	TTGAAAAAGT											2582
ATAAATAAAA	TGAGCAAAAG	TTGAA														2607

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 712 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Ser	Gln	Trp	Tyr	Glu	Leu	Gln	Gln	Leu	Asp	Ser	Lys	Phe	Leu	Glu
1				5					10					15	

Gln Val His Gln Leu Tyr Asp Asp Ser Phe Pro Met Glu Ile Arg Gln
 20 25 30
 Tyr Leu Ala Gln Trp Leu Glu Lys Gln Asp Trp Glu His Ala Ala Asn
 35 40 45
 Asp Val Ser Phe Ala Thr Ile Arg Phe His Asp Leu Leu Ser Gln Leu
 50 55 60
 Asp Asp Gln Tyr Ser Arg Phe Ser Leu Glu Asn Asn Phe Leu Leu Gln
 65 70 75 80
 His Asn Ile Arg Lys Ser Lys Arg Asn Leu Gln Asp Asn Phe Gln Glu
 85 90 95
 Asp Pro Ile Gln Met Ser Met Ile Ile Tyr Ser Cys Leu Lys Glu Glu
 100 105 110
 Arg Lys Ile Leu Glu Asn Ala Gln Arg Phe Asn Gln Ala Gln Ser Gly
 115 120 125
 Asn Ile Gln Ser Thr Val Met Leu Asp Lys Gln Lys Glu Leu Asp Ser
 130 135 140
 Lys Val Arg Asn Val Lys Asp Lys Val Met Cys Ile Glu His Glu Ile
 145 150 155 160
 Lys Ser Leu Glu Asp Leu Gln Asp Glu Tyr Asp Phe Lys Cys Lys Thr
 165 170 175
 Leu Gln Asn Arg Glu His Glu Thr Asn Gly Val Ala Lys Ser Asp Gln
 180 185 190
 Lys Gln Glu Gln Leu Leu Leu Lys Lys Met Tyr Leu Met Leu Asp Asn
 195 200 205
 Lys Arg Lys Glu Val Val His Lys Ile Ile Glu Leu Leu Asn Val Thr
 210 215 220
 Glu Leu Thr Gln Asn Ala Leu Ile Asn Asp Glu Leu Val Glu Trp Lys
 225 230 235 240
 Arg Arg Gln Gln Ser Ala Cys Ile Gly Gly Pro Pro Asn Ala Cys Leu
 245 250 255
 Asp Gln Leu Gln Asn Trp Phe Thr Ile Val Ala Glu Ser Leu Gln Gln
 260 265 270
 Val Arg Gln Gln Leu Lys Lys Leu Glu Glu Leu Glu Gln Lys Tyr Thr
 275 280 285
 Tyr Glu His Asp Pro Ile Thr Lys Asn Lys Gln Val Leu Trp Asp Arg
 290 295 300
 Thr Phe Ser Leu Phe Gln Gln Leu Ile Gln Ser Ser Phe Val Val Glu
 305 310 315 320
 Arg Gln Pro Cys Met Pro Thr His Pro Gln Arg Pro Leu Val Leu Lys
 325 330 335
 Thr Gly Val Gln Phe Thr Val Lys Leu Arg Leu Leu Val Lys Leu Gln
 340 345 350
 Glu Leu Asn Tyr Asn Leu Lys Val Lys Val Leu Phe Asp Lys Asp Val
 355 360 365
 Asn Glu Arg Asn Thr Val Lys Gly Phe Arg Lys Phe Asn Ile Leu Gly
 370 375 380

Thr 385	His	Thr	Lys	Val	Met 390	Asn	Met	Glu	Glu	Ser 395	Thr	Asn	Gly	Ser	Leu 400
Ala	Ala	Glu	Phe	Arg 405	His	Leu	Gln	Leu	Lys 410	Glu	Gln	Lys	Asn	Ala	Gly 415
Thr	Arg	Thr	Asn 420	Glu	Gly	Pro	Leu	Ile 425	Val	Thr	Glu	Glu	Leu 430	His	Ser
Leu	Ser	Phe 435	Glu	Thr	Gln	Leu	Cys 440	Gln	Pro	Gly	Leu	Val 445	Ile	Asp	Leu
Glu 450	Thr	Thr	Ser	Leu	Pro	Val 455	Val	Val	Ile	Ser	Asn 460	Val	Ser	Gln	Leu
Pro 465	Ser	Gly	Trp	Ala	Ser 470	Ile	Leu	Trp	Tyr	Asn 475	Met	Leu	Val	Ala	Glu 480
Pro	Arg	Asn	Leu	Ser 485	Phe	Phe	Leu	Thr	Pro	Pro	Cys	Ala	Arg	Trp	Ala 495
Gln	Leu	Ser	Glu 500	Val	Leu	Ser	Trp	Gln 505	Phe	Ser	Ser	Val	Thr 510	Lys	Arg
Gly	Leu	Asn 515	Val	Asp	Gln	Leu	Asn 520	Met	Leu	Gly	Glu	Lys 525	Leu	Leu	Gly
Pro 530	Asn	Ala	Ser	Pro	Asp	Gly 535	Leu	Ile	Pro	Trp	Thr 540	Arg	Phe	Cys	Lys
Glu 545	Asn	Ile	Asn	Asp	Lys 550	Asn	Phe	Pro	Phe	Trp 555	Leu	Trp	Ile	Glu	Ser 560
Ile	Leu	Glu	Leu	Ile 565	Lys	Lys	His	Leu	Leu 570	Pro	Leu	Trp	Asn	Asp 575	Gly
Cys	Ile	Met	Gly 580	Phe	Ile	Ser	Lys	Glu 585	Arg	Glu	Arg	Ala	Leu 590	Leu	Lys
Asp	Gln	Gln	Pro	Gly	Thr	Phe	Leu 600	Leu	Arg	Phe	Ser	Glu 605	Ser	Ser	Arg
Glu 610	Gly	Ala	Ile	Thr	Phe	Thr 615	Trp	Val	Glu	Arg	Ser	Gln 620	Asn	Gly	Gly
Glu 625	Pro	Asp	Phe	His	Ala 630	Val	Glu	Pro	Tyr	Thr 635	Lys	Lys	Glu	Leu	Ser 640
Ala	Val	Thr	Phe	Pro 645	Asp	Ile	Ile	Arg	Asn 650	Tyr	Lys	Val	Met	Ala	Ala 655
Glu	Asn	Ile	Pro	Glu	Asn	Pro	Leu	Lys 665	Tyr	Leu	Tyr	Pro	Asn 670	Ile	Asp
Lys	Asp	His 675	Ala	Phe	Gly	Lys	Tyr 680	Tyr	Ser	Arg	Pro	Lys 685	Glu	Ala	Pro
Glu 690	Pro	Met	Glu	Leu	Asp	Gly 695	Pro	Lys	Gly	Thr	Gly 700	Tyr	Ile	Lys	Thr
Glu 705	Leu	Ile	Ser	Val	Ser	Glu	Val								

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2277 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: both
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Mouse
(vii) IMMEDIATE SOURCE:
 (B) CLONE: Murine Stat91
(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 5..2251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CAGG ATG TCA CAG TGG TTC GAG CTT CAG CAG CTG GAC TCC AAG TTC CTG	49
Met Ser Gln Trp Phe Glu Leu Gln Gln Leu Asp Ser Lys Phe Leu	
1 5 10 15	
GAG CAG GTC CAC CAG CTG TAC GAT GAC AGT TTC CCC ATG GAA ATC AGA	97
Glu Gln Val His Gln Leu Tyr Asp Asp Ser Phe Pro Met Glu Ile Arg	
20 25 30	
CAG TAC CTG GCC CAG TGG CTG GAA AAG CAA GAC TGG GAG CAC GCT GCC	145
Gln Tyr Leu Ala Gln Trp Leu Glu Lys Gln Asp Trp Glu His Ala Ala	
35 40 45	
TAT GAT GTC TCG TTT GCG ACC ATC CGC TTC CAT GAC CTC CTC TCA CAG	193
Tyr Asp Val Ser Phe Ala Thr Ile Arg Phe His Asp Leu Leu Ser Gln	
50 55 60	
CTG GAC GAC CAG TAC AGC CGC TTT TCT CTG GAG AAT AAT TTC TTG TTG	241
Leu Asp Asp Gln Tyr Ser Arg Phe Ser Leu Glu Asn Asn Phe Leu Leu	
65 70 75	
CAG CAC AAC ATA CGG AAA AGC AAG CGT AAT CTC CAG GAT AAC TTC CAA	289
Gln His Asn Ile Arg Lys Ser Lys Arg Asn Leu Gln Asp Asn Phe Gln	
80 85 90 95	
GAA GAT CCC GTA CAG ATG TCC ATG ATC ATC TAC AAC TGT CTG AAG GAA	337
Glu Asp Pro Val Gln Met Ser Met Ile Ile Tyr Asn Cys Leu Lys Glu	
100 105 110	
GAA AGG AAG ATT TTG GAA AAT GCC CAA AGA TTT AAT CAG GCC CAG GAG	385
Glu Arg Lys Ile Leu Glu Asn Ala Gln Arg Phe Asn Gln Ala Gln Glu	
115 120 125	
GGA AAT ATT CAG AAC ACT GTG ATG TTA GAT AAA CAG AAG GAG CTG GAC	433
Gly Asn Ile Gln Asn Thr Val Met Leu Asp Lys Gln Lys Glu Leu Asp	
130 135 140	
AGT AAA GTC AGA AAT GTG AAG GAT CAA GTC ATG TGC ATA GAG CAG GAA	481
Ser Lys Val Arg Asn Val Lys Asp Gln Val Met Cys Ile Glu Gln Glu	
145 150 155	
ATC AAG ACC CTA GAA GAA TTA CAA GAT GAA TAT GAC TTT AAA TGC AAA	529
Ile Lys Thr Leu Glu Glu Leu Gln Asp Glu Tyr Asp Phe Lys Cys Lys	
160 165 170 175	
ACC TCT CAG AAC AGA GAA GGT GAA GCC AAT GGT GTG GCG AAG AGC GAC	577
Thr Ser Gln Asn Arg Glu Gly Glu Ala Asn Gly Val Ala Lys Ser Asp	
180 185 190	

CAA AAA CAG GAA CAG CTG CTG CTC CAC AAG ATG TTT TTA ATG CTT GAC Gln Lys Gln Glu Gln Leu Leu Leu His Lys Met Phe Leu Met Leu Asp 195 200 205	625
AAT AAG AGA AAG GAG ATA ATT CAC AAA ATC AGA GAG TTG CTG AAT TCC Asn Lys Arg Lys Glu Ile Ile His Lys Ile Arg Glu Leu Leu Asn Ser 210 215 220	673
ATC GAG CTC ACT CAG AAC ACT CTG ATT AAT GAC GAG CTC GTG GAG TGG Ile Glu Leu Thr Gln Asn Thr Leu Ile Asn Asp Glu Leu Val Glu Trp 225 230 235	721
AAG CGA AGG CAG CAG AGC GCC TGC ATC GGG GGA CCG CCC AAC GCC TGC Lys Arg Arg Gln Gln Ser Ala Cys Ile Gly Gly Pro Pro Asn Ala Cys 240 245 250 255	769
CTG GAT CAG CTG CAA ACG TGG TTC ACC ATT GTT GCA GAG ACC CTG CAG Leu Asp Gln Leu Gln Thr Trp Phe Thr Ile Val Ala Glu Thr Leu Gln 260 265 270	817
CAG ATC CGT CAG CAG CTT AAA AAG CTG GAG GAG TTG GAA CAG AAA TTC Gln Ile Arg Gln Gln Leu Lys Lys Leu Glu Glu Leu Glu Gln Lys Phe 275 280 285	865
ACC TAT GAG CCC GAC CCT ATT ACA AAA AAC AAG CAG GTG TTG TCA GAT Thr Tyr Glu Pro Asp Pro Ile Thr Lys Asn Lys Gln Val Leu Ser Asp 290 295 300	913
CGA ACC TTC CTC CTC TTC CAG CAG CTC ATT CAG AGC TCC TTC GTG GTA Arg Thr Phe Leu Leu Phe Gln Gln Leu Ile Gln Ser Ser Phe Val Val 305 310 315	961
GAA CGA CAG CCG TGC ATG CCC ACT CAC CCG CAG AGG CCC CTG GTC TTG Glu Arg Gln Pro Cys Met Pro Thr His Pro Gln Arg Pro Leu Val Leu 320 325 330 335	1009
AAG ACT GGG GTA CAG TTC ACT GTC AAG TCG AGA CTG TTG GTG AAA TTG Lys Thr Gly Val Gln Phe Thr Val Lys Ser Arg Leu Leu Val Lys Leu 340 345 350	1057
CAA GAG TCG AAT CTA TTA ACG AAA GTG AAA TGT CAC TTT GAC AAA GAT Gln Glu Ser Asn Leu Leu Thr Lys Val Lys Cys His Phe Asp Lys Asp 355 360 365	1105
GTG AAC GAG AAA AAC ACA GTT AAA GGA TTT CGG AAG TTC AAC ATC TTG Val Asn Glu Lys Asn Thr Val Lys Gly Phe Arg Lys Phe Asn Ile Leu 370 375 380	1153
GGT ACG CAC ACA AAA GTG ATG AAC ATG GAA GAA TCC ACC AAC GGA AGT Gly Thr His Thr Lys Val Met Asn Met Glu Glu Ser Thr Asn Gly Ser 385 390 395	1201
CTG GCA GCT GAG CTC CGA CAC CTG CAA CTG AAG GAA CAG AAA AAC GCT Leu Ala Ala Glu Leu Arg His Leu Gln Leu Lys Glu Gln Lys Asn Ala 400 405 410 415	1249
GGG AAC AGA ACT AAT GAG GGG CCT CTC ATT GTC ACC GAA GAA CTT CAC Gly Asn Arg Thr Asn Glu Gly Pro Leu Ile Val Thr Glu Glu Leu His 420 425 430	1297
TCT CTT AGC TTT GAA ACC CAG TTG TGC CAG CCA GGC TTG GTG ATT GAC Ser Leu Ser Phe Glu Thr Gln Leu Cys Gln Pro Gly Leu Val Ile Asp 435 440 445	1345
CTG GAG ACC ACC TCT CTT CCT GTC GTG GTG ATC TCC AAC GTC AGC CAG Leu Glu Thr Thr Ser Leu Pro Val Val Val Ile Ser Asn Val Ser Gln 450 455 460	1393

CTC Leu	CCC Pro	AGT Ser	GGC Gly	TGG Trp	GCG Ala	TCT Ser	ATC Ile	CTG Leu	TGG Trp	TAC Tyr	AAC Asn	ATG Met	CTG Leu	GTG Val	ACA Thr	1441
465 470 475																
GAG Glu	CCC Pro	AGG Arg	AAT Asn	CTC Leu	TCC Ser	TTC Phe	TTC Phe	CTG Leu	AAC Asn	CCC Pro	CCG Pro	TGC Cys	GCG Ala	TGG Trp	TGG Trp	1489
480 485 490 495																
TCC Ser	CAG Gln	CTC Leu	TCA Ser	GAG Glu	GTG Val	TTG Leu	AGT Ser	TGG Trp	CAG Gln	TTT Phe	TCA Ser	TCA Ser	GTC Val	ACC Thr	AAG Lys	1537
500 505 510																
AGA Arg	GGT Gly	CTG Leu	AAC Asn	GCA Ala	GAC Asp	CAG Gln	CTG Leu	AGC Ser	ATG Met	CTG Leu	GGA Gly	GAG Glu	AAG Lys	CTG Leu	CTG Leu	1585
515 520 525																
GGC Gly	CCT Pro	AAT Asn	GCT Ala	GGC Gly	CCT Pro	GAT Asp	GGT Gly	CTT Leu	ATT Ile	CCA Pro	TGG Trp	ACA Thr	AGG Arg	TTT Phe	TGT Cys	1633
530 535 540																
AAG Lys	GAA Glu	AAT Asn	ATT Ile	AAT Asn	GAT Asp	AAA Lys	AAT Asn	TTC Phe	TCC Ser	TTC Phe	TGG Trp	CCT Pro	TGG Trp	ATT Ile	GAC Asp	1681
545 550 555																
ACC Thr	ATC Ile	CTA Leu	GAG Glu	CTC Leu	ATT Ile	AAG Lys	AAC Asn	GAC Asp	CTG Leu	CTG Leu	TGC Cys	CTC Leu	TGG Trp	AAT Asn	GAT Asp	1729
560 565 570 575																
GGG Gly	TGC Cys	ATT Ile	ATG Met	GGC Gly	TTC Phe	ATC Ile	AGC Ser	AAG Lys	GAG Glu	CGA Arg	GAA Glu	CGC Arg	GCT Ala	CTG Leu	CTC Leu	1777
580 585 590																
AAG Lys	GAC Asp	CAG Gln	CAG Gln	CCA Pro	GGG Gly	ACG Thr	TTC Phe	CTG Leu	CTT Leu	AGA Arg	TTC Phe	AGT Ser	GAG Glu	AGC Ser	TCC Ser	1825
595 600 605																
CGG Arg	GAA Glu	GGG Gly	GCC Ala	ATC Ile	ACA Thr	TTC Phe	ACA Thr	TGG Trp	GTG Val	GAA Glu	CGG Arg	TCC Ser	CAG Gln	AAC Asn	GGA Gly	1873
610 615 620																
GGT Gly	GAA Glu	CCT Pro	GAC Asp	TTC Phe	CAT His	GCC Ala	GTG Val	GAG Glu	CCC Pro	TAC Tyr	ACG Thr	AAA Lys	AAA Lys	GAA Glu	CTT Leu	1921
625 630 635																
TCA Ser	GCT Ala	GTT Val	ACT Thr	TTC Phe	CCA Pro	GAT Asp	ATT Ile	ATT Ile	CGC Arg	AAC Asn	TAC Tyr	AAA Lys	GTC Val	ATG Met	GCT Ala	1969
640 645 650 655																
GCC Ala	GAG Glu	AAC Asn	ATA Ile	CCA Pro	GAG Glu	AAT Asn	CCC Pro	CTG Leu	AAG Lys	TAT Tyr	CTG Leu	TAC Tyr	CCC Pro	AAT Asn	ATT Ile	2017
660 665 670																
GAC Asp	AAA Lys	GAC Asp	CAC His	GCC Ala	TTT Phe	GGG Gly	AAG Lys	TAT Tyr	TAT Tyr	TCC Ser	AGA Arg	CCA Pro	AAG Lys	GAA Glu	GCA Ala	2065
675 680 685																
CCA Pro	GAA Glu	CCG Pro	ATG Met	GAG Glu	CTT Leu	GAC Asp	GAC Asp	CCT Pro	AAG Lys	CGA Arg	ACT Thr	GGA Gly	TAC Tyr	ATC Ile	AAG Lys	2113
690 695 700																
ACT Thr	GAG Glu	TTG Leu	ATT Ile	TCT Ser	GTG Val	TCT Ser	GAA Glu	GTC Val	CAC His	CCT Pro	TCT Ser	AGA Arg	CTT Leu	CAG Gln	ACC Thr	2161
705 710 715																
ACA Thr	GAC Asp	AAC Asn	CTG Leu	CTT Leu	CCC Pro	ATG Met	TCT Ser	CCA Pro	GAG Glu	GAG Glu	TTT Phe	GAT Asp	GAG Glu	ATG Met	TCC Ser	2209
720 725 730 735																

CGG ATA GTG GGC CCC GAA TTT GAC AGT ATG ATG AGC ACA GTA
Arg Ile Val Gly Pro Glu Phe Asp Ser Met Met Ser Thr Val

TAAACACGAA TTTCTCTCTG GCGACA

(2) INFORMATION FOR SEQ ID NO:8:

(A) LENGTH: 749 amino acids

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

Met 1	Ser	Gln	Trp	Phe 5	Glu	Leu	Gln	Gln	Leu 10	Asp	Ser	Lys	Phe	Leu 15	Glu
Gln	Val	His	Gln 20	Leu	Tyr	Asp	Asp	Ser 25	Phe	Pro	Met	Glu	Ile 30	Arg	Gln
Tyr	Leu	Ala 35	Gln	Trp	Leu	Glu	Lys 40	Gln	Asp	Trp	Glu	His 45	Ala	Ala	Tyr
Asp	Val 50	Ser	Phe	Ala	Thr	Ile 55	Arg	Phe	His	Asp	Leu 60	Leu	Ser	Gln	Leu
Asp 65	Asp	Gln	Tyr	Ser	Arg 70	Phe	Ser	Leu	Glu	Asn 75	Asn	Phe	Leu	Leu	Gln 80
His	Asn	Ile	Arg	Lys 85	Ser	Lys	Arg	Asn	Leu 90	Gln	Asp	Asn	Phe	Gln 95	Glu
Asp	Pro	Val 100	Gln	Met	Ser	Met	Ile	Ile 105	Tyr	Asn	Cys	Leu	Lys 110	Glu	Glu
Arg	Lys	Ile 115	Leu	Glu	Asn	Ala	Gln 120	Arg	Phe	Asn	Gln 125	Ala	Gln	Glu	Gly
Asn	Ile 130	Gln	Asn	Thr	Val	Met 135	Leu	Asp	Lys	Gln	Lys 140	Glu	Leu	Asp	Ser
Lys 145	Val	Arg	Asn	Val	Lys 150	Asp	Gln	Val	Met	Cys 155	Ile	Glu	Gln	Glu	Ile 160
Lys	Thr	Leu	Glu	Glu 165	Leu	Gln	Asp	Glu	Tyr 170	Asp	Phe	Lys	Cys	Lys 175	Thr
Ser	Gln	Asn	Arg 180	Glu	Gly	Glu	Ala	Asn 185	Gly	Val	Ala	Lys	Ser 190	Asp	Gln
Lys	Gln	Glu 195	Gln	Leu	Leu	Leu	His 200	Lys	Met	Phe	Leu	Met 205	Leu	Asp	Asn
Lys	Arg 210	Lys	Glu	Ile	Ile	His 215	Lys	Ile	Arg	Glu	Leu 220	Leu	Asn	Ser	Ile
Glu 225	Leu	Thr	Gln	Asn	Thr 230	Leu	Ile	Asn	Asp	Glu 235	Leu	Val	Glu	Trp	Lys 240
Arg	Arg	Gln	Gln	Ser 245	Ala	Cys	Ile	Gly	Gly 250	Pro	Pro	Asn	Ala	Cys 255	Leu
Asp	Gln	Leu	Gln 260	Thr	Trp	Phe	Thr	Ile 265	Val	Ala	Glu	Thr	Leu 270	Gln	Gln

Ile	Arg	Gln	Gln	Leu	Lys	Lys	Leu	Glu	Glu	Leu	Glu	Gln	Lys	Phe	Thr	275	280	285
Tyr	Glu	Pro	Asp	Pro	Ile	Thr	Lys	Asn	Lys	Gln	Val	Leu	Ser	Asp	Arg	290	295	300
Thr	Phe	Leu	Leu	Phe	Gln	Gln	Leu	Ile	Gln	Ser	Ser	Phe	Val	Val	Glu	305	310	315
Arg	Gln	Pro	Cys	Met	Pro	Thr	His	Pro	Gln	Arg	Pro	Leu	Val	Leu	Lys	325	330	335
Thr	Gly	Val	Gln	Phe	Thr	Val	Lys	Ser	Arg	Leu	Leu	Val	Lys	Leu	Gln	340	345	350
Glu	Ser	Asn	Leu	Leu	Thr	Lys	Val	Lys	Cys	His	Phe	Asp	Lys	Asp	Val	355	360	365
Asn	Glu	Lys	Asn	Thr	Val	Lys	Gly	Phe	Arg	Lys	Phe	Asn	Ile	Leu	Gly	370	375	380
Thr	His	Thr	Lys	Val	Met	Asn	Met	Glu	Glu	Ser	Thr	Asn	Gly	Ser	Leu	385	390	395
Ala	Ala	Glu	Leu	Arg	His	Leu	Gln	Leu	Lys	Glu	Gln	Lys	Asn	Ala	Gly	405	410	415
Asn	Arg	Thr	Asn	Glu	Gly	Pro	Leu	Ile	Val	Thr	Glu	Glu	Leu	His	Ser	420	425	430
Leu	Ser	Phe	Glu	Thr	Gln	Leu	Cys	Gln	Pro	Gly	Leu	Val	Ile	Asp	Leu	435	440	445
Glu	Thr	Thr	Ser	Leu	Pro	Val	Val	Val	Ile	Ser	Asn	Val	Ser	Gln	Leu	450	455	460
Pro	Ser	Gly	Trp	Ala	Ser	Ile	Leu	Trp	Tyr	Asn	Met	Leu	Val	Thr	Glu	465	470	475
Pro	Arg	Asn	Leu	Ser	Phe	Phe	Leu	Asn	Pro	Pro	Cys	Ala	Trp	Trp	Ser	485	490	495
Gln	Leu	Ser	Glu	Val	Leu	Ser	Trp	Gln	Phe	Ser	Ser	Val	Thr	Lys	Arg	500	505	510
Gly	Leu	Asn	Ala	Asp	Gln	Leu	Ser	Met	Leu	Gly	Glu	Lys	Leu	Leu	Gly	515	520	525
Pro	Asn	Ala	Gly	Pro	Asp	Gly	Leu	Ile	Pro	Trp	Thr	Arg	Phe	Cys	Lys	530	535	540
Glu	Asn	Ile	Asn	Asp	Lys	Asn	Phe	Ser	Phe	Trp	Pro	Trp	Ile	Asp	Thr	545	550	555
Ile	Leu	Glu	Leu	Ile	Lys	Asn	Asp	Leu	Leu	Cys	Leu	Trp	Asn	Asp	Gly	565	570	575
Cys	Ile	Met	Gly	Phe	Ile	Ser	Lys	Glu	Arg	Glu	Arg	Ala	Leu	Leu	Lys	580	585	590
Asp	Gln	Gln	Pro	Gly	Thr	Phe	Leu	Leu	Arg	Phe	Ser	Glu	Ser	Ser	Arg	595	600	605
Glu	Gly	Ala	Ile	Thr	Phe	Thr	Trp	Val	Glu	Arg	Ser	Gln	Asn	Gly	Gly	610	615	620
Glu	Pro	Asp	Phe	His	Ala	Val	Glu	Pro	Tyr	Thr	Lys	Lys	Glu	Leu	Ser	625	630	635

Ala Val Thr Phe Pro Asp Ile Ile Arg Asn Tyr Lys Val Met Ala Ala
645 650 655

Glu Asn Ile Pro Glu Asn Pro Leu Lys Tyr Leu Tyr Pro Asn Ile Asp
660 665 670

Lys Asp His Ala Phe Gly Lys Tyr Tyr Ser Arg Pro Lys Glu Ala Pro
675 680 685

Glu Pro Met Glu Leu Asp Asp Pro Lys Arg Thr Gly Tyr Ile Lys Thr
690 695 700

Glu Leu Ile Ser Val Ser Glu Val His Pro Ser Arg Leu Gln Thr Thr
705 710 715 720

Asp Asn Leu Leu Pro Met Ser Pro Glu Glu Phe Asp Glu Met Ser Arg
725 730 735

Ile Val Gly Pro Glu Phe Asp Ser Met Met Ser Thr Val
740 745

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Mouse
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: splenic/thymic
 - (B) CLONE: Murine 13sfl
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 34..2277
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGCCACTACC TGGACGGAGA GAGAGAGAGC AGC ATG TCT CAG TGG AAT CAA GTC	54
Met Ser Gln Trp Asn Gln Val	
1 5	
CAA CAA TTA GAA ATC AAG TTT TTG GAG CAA GTA GAT CAG TTC TAT GAT	102
Gln Gln Leu Glu Ile Lys Phe Leu Glu Gln Val Asp Gln Phe Tyr Asp	
10 15 20	
GAC AAC TTT CCT ATG GAA ATC CGG CAT CTG CTA GCT CAG TGG ATT GAG	150
Asp Asn Phe Pro Met Glu Ile Arg His Leu Leu Ala Gln Trp Ile Glu	
25 30 35	
ACT CAA GAC TGG GAA GTA GCT TCT AAC AAT GAA ACT ATG GCA ACA ATT	198
Thr Gln Asp Trp Glu Val Ala Ser Asn Asn Glu Thr Met Ala Thr Ile	
40 45 50 55	
CTG CTT CAA AAC TTA CTA ATA CAA TTG GAT GAA CAG TTG GGG CGG GTT	246
Leu Leu Gln Asn Leu Leu Ile Gln Leu Asp Glu Gln Leu Gly Arg Val	
60 65 70	

TCC	AAA	GAA	AAA	AAT	CTG	CTA	TTG	ATT	CAC	AAT	CTA	AAG	AGA	ATT	AGA	294
Ser	Lys	Glu	Lys	Asn	Leu	Leu	Leu	Ile	His	Asn	Leu	Lys	Arg	Ile	Arg	
			75					80					85			
AAA	GTT	CTT	CAG	GGC	AAG	TTT	CAT	GGA	AAT	CCA	ATG	CAT	GTA	GCT	GTG	342
Lys	Val	Leu	Gln	Gly	Lys	Phe	His	Gly	Asn	Pro	Met	His	Val	Ala	Val	
		90					95					100				
GTA	ATT	TCA	AAT	TGC	TTA	AGG	GAA	GAG	AGG	AGA	ATA	TTG	GCT	GCA	GCC	390
Val	Ile	Ser	Asn	Cys	Leu	Arg	Glu	Glu	Arg	Arg	Ile	Leu	Ala	Ala	Ala	
	105					110					115					
AAC	ATG	CCT	ATC	CAG	GGA	CCT	CTG	GAG	AAA	TCC	TTA	CAG	AGT	TCT	TCA	438
Asn	Met	Pro	Ile	Gln	Gly	Pro	Leu	Glu	Lys	Ser	Leu	Gln	Ser	Ser	Ser	
120					125					130					135	
GTT	TCT	GAA	AGA	CAA	AGG	AAT	GTG	GAA	CAC	AAA	GTG	TCT	GCC	ATT	AAA	486
Val	Ser	Glu	Arg	Gln	Arg	Asn	Val	Glu	His	Lys	Val	Ser	Ala	Ile	Lys	
			140						145				150			
AAC	AGT	GTG	CAG	ATG	ACA	GAA	CAA	GAT	ACC	AAA	TAC	TTA	GAA	GAC	CTG	534
Asn	Ser	Val	Gln	Met	Thr	Glu	Gln	Asp	Thr	Lys	Tyr	Leu	Glu	Asp	Leu	
			155					160					165			
CAA	GAT	GAG	TTT	GAC	TAC	AGG	TAT	AAA	ACA	ATT	CAG	ACA	ATG	GAT	CAG	582
Gln	Asp	Glu	Phe	Asp	Tyr	Arg	Tyr	Lys	Thr	Ile	Gln	Thr	Met	Asp	Gln	
		170					175					180				
GGT	GAC	AAA	AAC	AGT	ATC	CTG	GTG	AAC	CAG	GAA	GTT	TTG	ACA	CTG	CTG	630
Gly	Asp	Lys	Asn	Ser	Ile	Leu	Val	Asn	Gln	Glu	Val	Leu	Thr	Leu	Leu	
	185					190					195					
CAA	GAA	ATG	CTT	AAT	AGT	CTG	GAC	TTC	AAG	AGA	AAG	GAA	GCA	CTC	AGT	678
Gln	Glu	Met	Leu	Asn	Ser	Leu	Asp	Phe	Lys	Arg	Lys	Glu	Ala	Leu	Ser	
200					205					210					215	
AAG	ATG	ACG	CAG	ATA	GTG	AAC	GAG	ACA	GAC	CTG	CTC	ATG	AAC	AGC	ATG	726
Lys	Met	Thr	Gln	Ile	Val	Asn	Glu	Thr	Asp	Leu	Leu	Met	Asn	Ser	Met	
				220					225					230		
CTT	CTA	GAA	GAG	CTG	CAG	GAC	TGG	AAA	AAG	CGG	CAC	AGG	ATT	GCC	TGC	774
Leu	Leu	Glu	Glu	Leu	Gln	Asp	Trp	Lys	Lys	Arg	His	Arg	Ile	Ala	Cys	
			235					240					245			
ATT	GGT	GGC	CCG	CTC	CAC	AAT	GGG	CTG	GAC	CAG	CTT	CAG	AAC	TGC	TTT	822
Ile	Gly	Gly	Pro	Leu	His	Asn	Gly	Leu	Asp	Gln	Leu	Gln	Asn	Cys	Phe	
		250					255					260				
ACC	CTA	CTG	GCA	GAG	AGT	CTT	TTC	CAA	CTC	AGA	CAG	CAA	CTG	GAG	AAA	870
Thr	Leu	Leu	Ala	Glu	Ser	Leu	Phe	Gln	Leu	Arg	Gln	Gln	Leu	Glu	Lys	
		265				270					275					
CTA	CAG	GAG	CAA	TCT	ACT	AAA	ATG	ACC	TAT	GAA	GGG	GAT	CCC	ATC	CCT	918
Leu	Gln	Glu	Gln	Ser	Thr	Lys	Met	Thr	Tyr	Glu	Gly	Asp	Pro	Ile	Pro	
280					285					290					295	
GCT	CAA	AGA	GCA	CAC	CTC	CTG	GAA	AGA	GCT	ACC	TTC	CTG	ATC	TAC	AAC	966
Ala	Gln	Arg	Ala	His	Leu	Leu	Glu	Arg	Ala	Thr	Phe	Leu	Ile	Tyr	Asn	
				300					305					310		
CTT	TTC	AAG	AAC	TCA	TTT	GTG	GTC	GAG	CGA	CAC	GCA	TGC	ATG	CCA	ACG	1014
Leu	Phe	Lys	Asn	Ser	Phe	Val	Val	Glu	Arg	His	Ala	Cys	Met	Pro	Thr	
			315					320					325			
CAC	CCT	CAG	AGG	CCG	ATG	GTA	CTT	AAA	ACC	CTC	ATT	CAG	TTC	ACT	GTA	1062
His	Pro	Gln	Arg	Pro	Met	Val	Leu	Lys	Thr	Leu	Ile	Gln	Phe	Thr	Val	
		330					335					340				

AAA Lys	CTG Leu	AGA Arg	TTA Leu	CTA Leu	ATA Ile	AAA Lys	TTG Leu	CCG Pro	GAA Glu	CTA Leu	AAC Asn	TAT Tyr	CAG Gln	GTG Val	AAA Lys	1110
	345					350					355					
GTA Val	AAG Lys	GCG Ala	TCC Ser	ATT Ile	GAC Asp	AAG Lys	AAT Asn	GTT Val	TCA Ser	ACT Thr	CTA Leu	AGC Ser	AAT Asn	AGA Arg	AGA Arg	1158
360					365					370					375	
TTT Phe	GTG Val	CTT Leu	TGT Cys	GGA Gly	ACT Thr	CAC His	GTC Val	AAA Lys	GCT Ala	ATG Met	TCC Ser	AGT Ser	GAG Glu	GAA Glu	TCT Ser	1206
				380					385					390		
TCC Ser	AAT Asn	GGG Gly	AGC Ser	CTC Leu	TCA Ser	GTG Val	GAG Glu	TTA Leu	GAC Asp	ATT Ile	GCA Ala	ACC Thr	CAA Gln	GGA Gly	GAT Asp	1254
			395					400					405			
GAA Glu	GTG Val	CAG Gln	TAC Tyr	TGG Trp	AGT Ser	AAA Lys	GGA Gly	AAC Asn	GAG Glu	GGC Gly	TGC Cys	CAC His	ATG Met	GTG Val	ACA Thr	1302
		410					415					420				
GAG Glu	GAG Glu	TTG Leu	CAT His	TCC Ser	ATA Ile	ACC Thr	TTT Phe	GAG Glu	ACC Thr	CAG Gln	ATC Ile	TGC Cys	CTC Leu	TAT Tyr	GGC Gly	1350
	425					430					435					
CTC Leu	ACC Thr	ATT Ile	AAC Asn	CTA Leu	GAG Glu	ACC Thr	AGC Ser	TCA Ser	TTA Leu	CCT Pro	GTC Val	GTG Val	ATG Met	ATT Ile	TCT Ser	1398
440					445					450					455	
AAT Asn	GTC Val	AGC Ser	CAA Gln	CTA Leu	CCT Pro	AAT Asn	GCA Ala	TGG Trp	GCA Ala	TCC Ser	ATC Ile	ATT Ile	TGG Trp	TAC Tyr	AAT Asn	1446
				460					465					470		
GTA Val	TCA Ser	ACT Thr	AAC Asn	GAC Asp	TCC Ser	CAG Gln	AAC Asn	TTG Leu	GTT Val	TTC Phe	TTT Phe	AAT Asn	AAC Asn	CCT Pro	CCA Pro	1494
			475					480					485			
TCT Ser	GTC Val	ACT Thr	TTG Leu	GGC Gly	CAA Gln	CTC Leu	CTG Leu	GAA Glu	GTG Val	ATG Met	AGC Ser	TGG Trp	CAA Gln	TTT Phe	TCA Ser	1542
		490					495					500				
TCC Ser	TAT Tyr	GTC Val	GGT Gly	CGT Arg	GGC Gly	CTT Leu	AAT Asn	TCA Ser	GAG Glu	CAG Gln	CTC Leu	AAC Asn	ATG Met	CTG Leu	GCA Ala	1590
	505					510					515					
GAG Glu	AAG Lys	CTC Leu	ACA Thr	GTT Val	CAG Gln	TCT Ser	AAC Asn	TAC Tyr	AAT Asn	GAT Asp	GGT Gly	CAC His	CTC Leu	ACC Thr	TGG Trp	1638
520					525					530					535	
GCC Ala	AAG Lys	TTC Phe	TGC Cys	AAG Lys	GAA Glu	CAT His	TTG Leu	CCT Pro	GGC Gly	AAA Lys	ACA Thr	TTT Phe	ACC Thr	TTC Phe	TGG Trp	1686
				540					545					550		
ACT Thr	TGG Trp	CTT Leu	GAA Glu	GCA Ala	ATA Ile	TTG Leu	GAC Asp	CTA Leu	ATT Ile	AAA Lys	AAA Lys	CAT His	ATT Ile	CTT Leu	CCC Pro	1734
			555					560					565			
CTC Leu	TGG Trp	ATT Ile	GAT Asp	GGG Gly	TAC Tyr	ATC Ile	ATG Met	GGA Gly	TTT Phe	GTT Val	AGT Ser	AAA Lys	GAG Glu	AAG Lys	GAA Glu	1782
		570					575					580				
CGG Arg	CTT Leu	CTG Leu	CTC Leu	AAA Lys	GAT Asp	AAA Lys	ATG Met	CCT Pro	GGG Gly	ACA Thr	TTT Phe	TTG Leu	TTA Leu	AGA Arg	TTC Phe	1830
	585					590					595					
AGT Ser	GAG Glu	AGC Ser	CAT His	CTT Leu	GGA Gly	GGG Gly	ATA Ile	ACC Thr	TTC Phe	ACC Thr	TGG Trp	GTG Val	GAC Asp	CAA Gln	TCT Ser	1878
600					605					610					615	

GAA AAT GGA GAA GTG AGA TTC CAC TCT GTA GAA CCC TAC AAC AAA GGG Glu Asn Gly Glu Val Arg Phe His Ser Val Glu Pro Tyr Asn Lys Gly 620 625 630	1926
AGA CTG TCG GCT CTG GCC TTC GCT GAC ATC CTG CGA GAC TAC AAG GTT Arg Leu Ser Ala Leu Ala Phe Ala Asp Ile Leu Arg Asp Tyr Lys Val 635 640 645	1974
ATC ATG GCT GAA AAC ATC CCT GAA AAC CCT CTG AAG TAC CTC TAC CCT Ile Met Ala Glu Asn Ile Pro Glu Asn Pro Leu Lys Tyr Leu Tyr Pro 650 655 660	2022
GAC ATT CCC AAA GAC AAA GCC TTT GGC AAA CAC TAC AGC TCC CAG CCG Asp Ile Pro Lys Asp Lys Ala Phe Gly Lys His Tyr Ser Ser Gln Pro 665 670 675	2070
TGC GAA GTC TCA AGA CCA ACC GAA CGG GGA GAC AAG GGT TAC GTC CCC Cys Glu Val Ser Arg Pro Thr Glu Arg Gly Asp Lys Gly Tyr Val Pro 680 685 690 695	2118
TCT GTT TTT ATC CCC ATT TCA ACA ATC CGA AGC GAT TCC ACG GAG CCA Ser Val Phe Ile Pro Ile Ser Thr Ile Arg Ser Asp Ser Thr Glu Pro 700 705 710	2166
CAA TCT CCT TCA GAC CTT CTC CCC ATG TCT CCA AGT GCA TAT GCT GTG Gln Ser Pro Ser Asp Leu Leu Pro Met Ser Pro Ser Ala Tyr Ala Val 715 720 725	2214
CTG AGA GAA AAC CTG AGC CCA ACG ACA ATT GAA ACT GCA ATG AAT TCC Leu Arg Glu Asn Leu Ser Pro Thr Ile Glu Thr Ala Met Asn Ser 730 735 740	2262
CCA TAT TCT GCT GAA TGACGGTGCA AACGGACACT TTAAAGAAGG AAGCAGATGA Pro Tyr Ser Ala Glu	2317
AAC TGAGAGAG TGTTCTTTAC CATAGATCAC AATTTATTTC TTCGGCTTTG TAAATACC	2375

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Ser Gln Trp Asn Gln Val Gln Gln Leu Glu Ile Lys Phe Leu Glu 1 5 10 15
Gln Val Asp Gln Phe Tyr Asp Asp Asn Phe Pro Met Glu Ile Arg His 20 25 30
Leu Leu Ala Gln Trp Ile Glu Thr Gln Asp Trp Glu Val Ala Ser Asn 35 40 45
Asn Glu Thr Met Ala Thr Ile Leu Leu Gln Asn Leu Leu Ile Gln Leu 50 55 60
Asp Glu Gln Leu Gly Arg Val Ser Lys Glu Lys Asn Leu Leu Leu Ile 65 70 75 80
His Asn Leu Lys Arg Ile Arg Lys Val Leu Gln Gly Lys Phe His Gly 85 90 95

Asn	Pro	Met	His	Val	Ala	Val	Val	Ile	Ser	Asn	Cys	Leu	Arg	Glu	Glu		
			100					105					110				
Arg	Arg	Ile	Leu	Ala	Ala	Ala	Asn	Met	Pro	Ile	Gln	Gly	Pro	Leu	Glu		
		115					120					125					
Lys	Ser	Leu	Gln	Ser	Ser	Ser	Val	Ser	Glu	Arg	Gln	Arg	Asn	Val	Glu		
	130					135					140						
His	Lys	Val	Ser	Ala	Ile	Lys	Asn	Ser	Val	Gln	Met	Thr	Glu	Gln	Asp		
145					150					155					160		
Thr	Lys	Tyr	Leu	Glu	Asp	Leu	Gln	Asp	Glu	Phe	Asp	Tyr	Arg	Tyr	Lys		
			165						170					175			
Thr	Ile	Gln	Thr	Met	Asp	Gln	Gly	Asp	Lys	Asn	Ser	Ile	Leu	Val	Asn		
			180					185					190				
Gln	Glu	Val	Leu	Thr	Leu	Leu	Gln	Glu	Met	Leu	Asn	Ser	Leu	Asp	Phe		
		195					200					205					
Lys	Arg	Lys	Glu	Ala	Leu	Ser	Lys	Met	Thr	Gln	Ile	Val	Asn	Glu	Thr		
	210					215					220						
Asp	Leu	Leu	Met	Asn	Ser	Met	Leu	Leu	Glu	Glu	Leu	Gln	Asp	Trp	Lys		
225					230					235					240		
Lys	Arg	His	Arg	Ile	Ala	Cys	Ile	Gly	Gly	Pro	Leu	His	Asn	Gly	Leu		
				245					250					255			
Asp	Gln	Leu	Gln	Asn	Cys	Phe	Thr	Leu	Leu	Ala	Glu	Ser	Leu	Phe	Gln		
			260					265					270				
Leu	Arg	Gln	Gln	Leu	Glu	Lys	Leu	Gln	Glu	Gln	Ser	Thr	Lys	Met	Thr		
		275					280					285					
Tyr	Glu	Gly	Asp	Pro	Ile	Pro	Ala	Gln	Arg	Ala	His	Leu	Leu	Glu	Arg		
	290					295					300						
Ala	Thr	Phe	Leu	Ile	Tyr	Asn	Leu	Phe	Lys	Asn	Ser	Phe	Val	Val	Glu		
305					310					315					320		
Arg	His	Ala	Cys	Met	Pro	Thr	His	Pro	Gln	Arg	Pro	Met	Val	Leu	Lys		
				325					330					335			
Thr	Leu	Ile	Gln	Phe	Thr	Val	Lys	Leu	Arg	Leu	Leu	Ile	Lys	Leu	Pro		
			340					345					350				
Glu	Leu	Asn	Tyr	Gln	Val	Lys	Val	Lys	Ala	Ser	Ile	Asp	Lys	Asn	Val		
		355					360					365					
Ser	Thr	Leu	Ser	Asn	Arg	Arg	Phe	Val	Leu	Cys	Gly	Thr	His	Val	Lys		
	370					375					380						
Ala	Met	Ser	Ser	Glu	Glu	Ser	Ser	Asn	Gly	Ser	Leu	Ser	Val	Glu	Leu		
385					390					395					400		
Asp	Ile	Ala	Thr	Gln	Gly	Asp	Glu	Val	Gln	Tyr	Trp	Ser	Lys	Gly	Asn		
				405					410					415			
Glu	Gly	Cys	His	Met	Val	Thr	Glu	Glu	Leu	His	Ser	Ile	Thr	Phe	Glu		
			420					425					430				
Thr	Gln	Ile	Cys	Leu	Tyr	Gly	Leu	Thr	Ile	Asn	Leu	Glu	Thr	Ser	Ser		
		435					440					445					
Leu	Pro	Val	Val	Met	Ile	Ser	Asn	Val	Ser	Gln	Leu	Pro	Asn	Ala	Trp		
	450					455					460						

Ala	Ser	Ile	Ile	Trp	Tyr	Asn	Val	Ser	Thr	Asn	Asp	Ser	Gln	Asn	Leu	465	470	475	480
Val	Phe	Phe	Asn	Asn	Pro	Pro	Ser	Val	Thr	Leu	Gly	Gln	Leu	Leu	Glu		485	490	495
Val	Met	Ser	Trp	Gln	Phe	Ser	Ser	Tyr	Val	Gly	Arg	Gly	Leu	Asn	Ser	500	505	510	
Glu	Gln	Leu	Asn	Met	Leu	Ala	Glu	Lys	Leu	Thr	Val	Gln	Ser	Asn	Tyr	515	520	525	
Asn	Asp	Gly	His	Leu	Thr	Trp	Ala	Lys	Phe	Cys	Lys	Glu	His	Leu	Pro	530	535	540	
Gly	Lys	Thr	Phe	Thr	Phe	Trp	Thr	Trp	Leu	Glu	Ala	Ile	Leu	Asp	Leu	545	550	555	560
Ile	Lys	Lys	His	Ile	Leu	Pro	Leu	Trp	Ile	Asp	Gly	Tyr	Ile	Met	Gly	565	570	575	
Phe	Val	Ser	Lys	Glu	Lys	Glu	Arg	Leu	Leu	Leu	Lys	Asp	Lys	Met	Pro	580	585	590	
Gly	Thr	Phe	Leu	Leu	Arg	Phe	Ser	Glu	Ser	His	Leu	Gly	Gly	Ile	Thr	595	600	605	
Phe	Thr	Trp	Val	Asp	Gln	Ser	Glu	Asn	Gly	Glu	Val	Arg	Phe	His	Ser	610	615	620	
Val	Glu	Pro	Tyr	Asn	Lys	Gly	Arg	Leu	Ser	Ala	Leu	Ala	Phe	Ala	Asp	625	630	635	640
Ile	Leu	Arg	Asp	Tyr	Lys	Val	Ile	Met	Ala	Glu	Asn	Ile	Pro	Glu	Asn	645	650	655	
Pro	Leu	Lys	Tyr	Leu	Tyr	Pro	Asp	Ile	Pro	Lys	Asp	Lys	Ala	Phe	Gly	660	665	670	
Lys	His	Tyr	Ser	Ser	Gln	Pro	Cys	Glu	Val	Ser	Arg	Pro	Thr	Glu	Arg	675	680	685	
Gly	Asp	Lys	Gly	Tyr	Val	Pro	Ser	Val	Phe	Ile	Pro	Ile	Ser	Thr	Ile	690	695	700	
Arg	Ser	Asp	Ser	Thr	Glu	Pro	Gln	Ser	Pro	Ser	Asp	Leu	Leu	Pro	Met	705	710	715	720
Ser	Pro	Ser	Ala	Tyr	Ala	Val	Leu	Arg	Glu	Asn	Leu	Ser	Pro	Thr	Thr	725	730	735	
Ile	Glu	Thr	Ala	Met	Asn	Ser	Pro	Tyr	Ser	Ala	Glu					740	745		

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2869 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mouse

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: splenic/thymic

(B) CLONE: Murine 19sf6

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 69..2378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCCGCGACCA GCCAGGCCGG CCAGTCGGGC TCAGCCCGGA GACAGTCGAG ACCCCTGACT	60
GCAGCAGG ATG GCT CAG TGG AAC CAG CTG CAG CAG CTG GAC ACA CGC TAC	110
Met Ala Gln Trp Asn Gln Leu Gln Gln Leu Asp Thr Arg Tyr	
1 5 10	
CTG AAG CAG CTG CAC CAG CTG TAC AGC GAC ACG TTC CCC ATG GAG CTG	158
Leu Lys Gln Leu His Gln Leu Tyr Ser Asp Thr Phe Pro Met Glu Leu	
15 20 25 30	
CGG CAG TTC CTG GCA CCT TGG ATT GAG AGT CAA GAC TGG GCA TAT GCA	206
Arg Gln Phe Leu Ala Pro Trp Ile Glu Ser Gln Asp Trp Ala Tyr Ala	
35 40 45	
GCC AGC AAA GAG TCA CAT GCC ACG TTG GTG TTT CAT AAT CTC TTG GGT	254
Ala Ser Lys Glu Ser His Ala Thr Leu Val Phe His Asn Leu Leu Gly	
50 55 60	
GAA ATT GAC CAG CAA TAT AGC CGA TTC CTG CAA GAG TCC AAT GTC CTC	302
Glu Ile Asp Gln Gln Tyr Ser Arg Phe Leu Gln Glu Ser Asn Val Leu	
65 70 75	
TAT CAG CAC AAC CTT CGA AGA ATC AAG CAG TTT CTG CAG AGC AGG TAT	350
Tyr Gln His Asn Leu Arg Arg Ile Lys Gln Phe Leu Gln Ser Arg Tyr	
80 85 90	
CTT GAG AAG CCA ATG GAA ATT GCC CGG ATC GTG GCC CGA TGC CTG TGG	398
Leu Glu Lys Pro Met Glu Ile Ala Arg Ile Val Ala Arg Cys Leu Trp	
95 100 105 110	
GAA GAG TCT CGC CTC CTC CAG ACG GCA GCC ACG GCA GCC CAG CAA GGG	446
Glu Glu Ser Arg Leu Leu Gln Thr Ala Ala Thr Ala Ala Gln Gln Gly	
115 120 125	
GGC CAG GCC AAC CAC CCA ACA GCC GCC GTA GTG ACA GAG AAG CAG CAG	494
Gly Gln Ala Asn His Pro Thr Ala Ala Val Val Thr Glu Lys Gln Gln	
130 135 140	
ATG TTG GAG CAG CAT CTT CAG GAT GTC CGG AAG CGA GTG CAG GAT CTA	542
Met Leu Glu Gln His Leu Gln Asp Val Arg Lys Arg Val Gln Asp Leu	
145 150 155	
GAA CAG AAA ATG AAG GTG GTG GAG AAC CTC CAG GAC GAC TTT GAT TTC	590
Glu Gln Lys Met Lys Val Val Glu Asn Leu Gln Asp Asp Phe Asp Phe	
160 165 170	
AAC TAC AAA ACC CTC AAG AGC CAA GGA GAC ATG CAG GAT CTG AAT GGA	638
Asn Tyr Lys Thr Leu Lys Ser Gln Gly Asp Met Gln Asp Leu Asn Gly	
175 180 185 190	
AAC AAC CAG TCT GTG ACC AGA CAG AAG ATG CAG CAG CTG GAA CAG ATG	686
Asn Asn Gln Ser Val Thr Arg Gln Lys Met Gln Gln Leu Glu Gln Met	
195 200 205	

CTC	ACA	GCC	CTG	GAC	CAG	ATG	CGG	AGA	AGC	ATT	GTG	AGT	GAG	CTG	GCG	734
Leu	Thr	Ala	Leu	Asp	Gln	Met	Arg	Arg	Ser	Ile	Val	Ser	Glu	Leu	Ala	
			210					215					220			
GGG	CTC	TTG	TCA	GCA	ATG	GAG	TAC	GTG	CAG	AAG	ACA	CTG	ACT	GAT	GAA	782
Gly	Leu	Leu	Ser	Ala	Met	Glu	Tyr	Val	Gln	Lys	Thr	Leu	Thr	Asp	Glu	
		225					230					235				
GAG	CTG	GCT	GAC	TGG	AAG	AGG	CGG	CCA	GAG	ATC	GCG	TGC	ATC	GGA	GCG	830
Glu	Leu	Ala	Asp	Trp	Lys	Arg	Arg	Pro	Glu	Ile	Ala	Cys	Ile	Gly	Gly	
	240					245					250					
CCT	CCC	AAC	ATC	TGC	CTG	GAC	CGT	CTG	GAA	AAC	TGG	ATA	ACT	TCA	TTA	878
Pro	Pro	Asn	Ile	Cys	Leu	Asp	Arg	Leu	Glu	Asn	Trp	Ile	Thr	Ser	Leu	
255					260					265					270	
GCA	GAA	TCT	CAA	CTT	CAG	ACC	CGC	CAA	CAA	ATT	AAG	AAA	CTG	GAG	GAG	926
Ala	Glu	Ser	Gln	Leu	Gln	Thr	Arg	Gln	Gln	Ile	Lys	Lys	Leu	Glu	Glu	
				275					280					285		
CTG	CAG	CAG	AAA	GTG	TCC	TAC	AAG	GGC	GAC	CCT	ATC	GTG	CAG	CAC	CGG	974
Leu	Gln	Gln	Lys	Val	Ser	Tyr	Lys	Gly	Asp	Pro	Ile	Val	Gln	His	Arg	
			290					295					300			
CCC	ATG	CTG	GAG	GAG	AGG	ATC	GTG	GAG	CTG	TTC	AGA	AAC	TTA	ATG	AAG	1022
Pro	Met	Leu	Glu	Glu	Arg	Ile	Val	Glu	Leu	Phe	Arg	Asn	Leu	Met	Lys	
		305					310					315				
AGT	GCC	TTC	GTG	GTG	GAG	CGG	CAG	CCC	TGC	ATG	CCC	ATG	CAC	CCG	GAC	1070
Ser	Ala	Phe	Val	Val	Glu	Arg	Gln	Pro	Cys	Met	Pro	Met	His	Pro	Asp	
	320					325					330					
CGG	CCC	TTA	GTC	ATC	AAG	ACT	GGT	GTC	CAG	TTT	ACC	ACG	AAA	GTC	AGG	1118
Arg	Pro	Leu	Val	Ile	Lys	Thr	Gly	Val	Gln	Phe	Thr	Thr	Lys	Val	Arg	
335					340					345					350	
TTG	CTG	GTC	AAA	TTT	CCT	GAG	TTG	AAT	TAT	CAG	CTT	AAA	ATT	AAA	GTG	1166
Leu	Leu	Val	Lys	Phe	Pro	Glu	Leu	Asn	Tyr	Gln	Leu	Lys	Ile	Lys	Val	
				355					360					365		
TGC	ATT	GAT	AAA	GAC	TCT	GGG	GAT	GTT	GCT	GCC	CTC	AGA	GGG	TCT	CGG	1214
Cys	Ile	Asp	Lys	Asp	Ser	Gly	Asp	Val	Ala	Ala	Leu	Arg	Gly	Ser	Arg	
			370					375					380			
AAA	TTT	AAC	ATT	CTG	GGC	ACG	AAC	ACA	AAA	GTG	ATG	AAC	ATG	GAG	GAG	1262
Lys	Phe	Asn	Ile	Leu	Gly	Thr	Asn	Thr	Lys	Val	Met	Asn	Met	Glu	Glu	
		385					390					395				
TCT	AAC	AAC	GGC	AGC	CTG	TCT	GCA	GAG	TTC	AAG	CAC	CTG	ACC	CTT	AGG	1310
Ser	Asn	Asn	Gly	Ser	Leu	Ser	Ala	Glu	Phe	Lys	His	Leu	Thr	Leu	Arg	
	400					405					410					
GAG	CAG	AGA	TGT	GGG	AAT	GGA	GGC	CGT	GCC	AAT	TGT	GAT	GCC	TCC	TTG	1358
Glu	Gln	Arg	Cys	Gly	Asn	Gly	Gly	Arg	Ala	Asn	Cys	Asp	Ala	Ser	Leu	
415					420					425					430	
ATC	GTG	ACT	GAG	GAG	CTG	CAC	CTG	ATC	ACC	TTC	GAG	ACT	GAG	GTG	TAC	1406
Ile	Val	Thr	Glu	Glu	Leu	His	Leu	Ile	Thr	Phe	Glu	Thr	Glu	Val	Tyr	
				435					440					445		
CAC	CAA	GGC	CTC	AAG	ATT	GAC	CTA	GAG	ACC	CAC	TCC	TTG	CCA	GTT	GTG	1454
His	Gln	Gly	Leu	Lys	Ile	Asp	Leu	Glu	Thr	His	Ser	Leu	Pro	Val	Val	
			450					455					460			
GTG	ATC	TCC	AAC	ATC	TGT	CAG	ATG	CCA	AAT	GCT	TGG	GCA	TCA	ATC	CTG	1502
Val	Ile	Ser	Asn	Ile	Cys	Gln	Met	Pro	Asn	Ala	Trp	Ala	Ser	Ile	Leu	
		465					470					475				

TGG Trp	TAT Tyr	AAC Asn	ATG Met	CTG Leu	ACC Thr	AAT Asn	AAC Asn	CCC Pro	AAG Lys	AAC Asn	GTG Val	AAC Asn	TTC Phe	TTC Phe	ACT Thr	1550
480 485 490																
AAG Lys	CCG Pro	CCA Pro	ATT Ile	GGA Gly	ACC Thr	TGG Trp	GAC Asp	CAA Gln	GTG Val	GCC Ala	GAG Glu	GTG Val	CTC Leu	AGC Ser	TGG Trp	1598
495 500 505																
CAG Gln	TTC Phe	TCG Ser	TCC Ser	ACC Thr	ACC Thr	AAG Lys	CGA Arg	GGG Gly	CTG Leu	AGC Ser	ATC Ile	GAG Glu	CAG Gln	CTG Leu	ACA Thr	1646
515 520 525																
ACG Thr	CTG Leu	GCT Ala	GAG Glu	AAG Lys	CTC Leu	CTA Leu	GGG Gly	CCT Pro	GGT Gly	GTG Val	AAC Asn	TAC Tyr	TCA Ser	GGG Gly	TGT Cys	1694
530 535 540																
CAG Gln	ATC Ile	ACA Thr	TGG Trp	GCT Ala	AAA Lys	TTC Phe	TGC Cys	AAA Lys	GAA Glu	AAC Asn	ATG Met	GCT Ala	GGC Gly	AAG Lys	GGC Gly	1742
545 550 555																
TTC Phe	TCC Ser	TTC Phe	TGG Trp	GTC Val	TGG Trp	CTA Leu	GAC Asp	AAT Asn	ATC Ile	ATC Ile	GAC Asp	CTT Leu	GTG Val	AAA Lys	AAG Lys	1790
560 565 570																
TAT Tyr	ATC Ile	TTG Leu	GCC Ala	CTT Leu	TGG Trp	AAT Asn	GAA Glu	GGG Gly	TAC Tyr	ATC Ile	ATG Met	GGT Gly	TTC Phe	ATC Ile	AGC Ser	1838
575 580 585 590																
AAG Lys	GAG Glu	CGG Arg	GAG Glu	CGG Arg	GCC Ala	ATC Ile	CTA Leu	AGC Ser	ACA Thr	AAG Lys	CCC Pro	CCG Pro	GGC Gly	ACC Thr	TTC Phe	1886
595 600 605																
CTA Leu	CTG Leu	CGC Arg	TTC Phe	AGC Ser	GAG Glu	AGC Ser	AGC Ser	AAA Lys	GAA Glu	GGA Gly	GGG Gly	GTC Val	ACT Thr	TTC Phe	ACT Thr	1934
610 615 620																
TGG Trp	GTG Val	GAA Glu	AAG Lys	GAC Asp	ATC Ile	AGT Ser	GGC Gly	AAG Lys	ACC Thr	CAG Gln	ATC Ile	CAG Gln	TCT Ser	GTA Val	GAG Glu	1982
625 630 635																
CCA Pro	TAC Tyr	ACC Thr	AAG Lys	CAG Gln	CAG Gln	CTG Leu	AAC Asn	AAC Asn	ATG Met	TCA Ser	TTT Phe	GCT Ala	GAA Glu	ATC Ile	ATC Ile	2030
640 645 650																
ATG Met	GGC Gly	TAT Tyr	AAG Lys	ATC Ile	ATG Met	GAT Asp	GCG Ala	ACC Thr	AAC Asn	ATC Ile	CTG Leu	GTG Val	TCT Ser	CCA Pro	CTT Leu	2078
655 660 665 670																
GTC Val	TAC Tyr	CTC Leu	TAC Tyr	CCC Pro	GAC Asp	ATT Ile	CCC Pro	AAG Lys	GAG Glu	GAG Glu	GCA Ala	TTT Phe	GGA Gly	AAG Lys	TAC Tyr	2126
675 680 685																
TGT Cys	AGG Arg	CCC Pro	GAG Glu	AGC Ser	CAG Gln	GAG Glu	CAC His	CCC Pro	GAA Glu	GCC Ala	GAC Asp	CCA Pro	GGT Gly	AGT Ser	GCT Ala	2174
690 695 700																
GCC Ala	CCG Pro	TAC Tyr	CTG Leu	AAG Lys	ACC Thr	AAG Lys	TTC Phe	ATC Ile	TGT Cys	GTG Val	ACA Thr	CCA Pro	ACG Thr	ACC Thr	TGC Cys	2222
705 710 715																
AGC Ser	AAT Asn	ACC Thr	ATT Ile	GAC Asp	CTG Leu	CCG Pro	ATG Met	TCC Ser	CCC Pro	CGC Arg	ACT Thr	TTA Leu	GAT Asp	TCA Ser	TTG Leu	2270
720 725 730																
ATG Met	CAG Gln	TTT Phe	GGA Gly	AAT Asn	AAC Asn	GGT Gly	GAA Glu	GGT Gly	GCT Ala	GAG Glu	CCC Pro	TCA Ser	GCA Ala	GGA Gly	GGG Gly	2318
735 740 745 750																

CAG TTT GAG TCG CTC ACG TTT GAC ATG GAT CTG ACC TCG GAG TGT GCT	2366
Gln Phe Glu Ser Leu Thr Phe Asp Met Asp Leu Thr Ser Glu Cys Ala	
755 760 765	
ACC TCC CCC ATG TGAGGAGCTG AAACCAGAAG CTGCAGAGAC GTGACTTGAG	2418
Thr Ser Pro Met	
770	
ACACCTGCCC CGTGCTCCAC CCCTAAGCAG CCGAACCCCA TATCGTCTGA AACTCCTAAC	2478
TTTGTGGTTC CAGATTTTTT TTTTAAATTT CCTACTTCTG CTATCTTTGG GCAATCTGGG	2538
CACTTTTTTAA AAGAGAGAAA TGAGTGAGTG TGGGTGATAA ACTGTTATGT AAAGAGGAGA	2598
GACCTCTGAG TCTGGGGATG GGGCTGAGAG CAGAAGGGAG GCAAAGGGGA ACACCTCCTG	2658
TCCTGCCCCG CTGCCCTCCT TTTTCAGCAG CTCGGGGGTT GGTGTGTTAGA CAAGTGCCTC	2718
CTGGTGCCCA TGGCTACCTG TTGCCCCACT CTGTGAGCTG ATACCCCAT T CTGGGAACTC	2778
CTGGCTCTGC ACTTTCAACC TTGCTAATAT CCACATAGAA GCTAGGACTA AGCCCAGGAG	2838
GTTCTCTTTT AAATTAAAAA AAAAAAAAAA A	2869

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 770 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Ala	Gln	Trp	Asn	Gln	Leu	Gln	Gln	Leu	Asp	Thr	Arg	Tyr	Leu	Lys
1				5					10					15	
Gln	Leu	His	Gln	Leu	Tyr	Ser	Asp	Thr	Phe	Pro	Met	Glu	Leu	Arg	Gln
		20						25					30		
Phe	Leu	Ala	Pro	Trp	Ile	Glu	Ser	Gln	Asp	Trp	Ala	Tyr	Ala	Ala	Ser
		35					40					45			
Lys	Glu	Ser	His	Ala	Thr	Leu	Val	Phe	His	Asn	Leu	Leu	Gly	Glu	Ile
	50					55					60				
Asp	Gln	Gln	Tyr	Ser	Arg	Phe	Leu	Gln	Glu	Ser	Asn	Val	Leu	Tyr	Gln
	65				70					75					80
His	Asn	Leu	Arg	Arg	Ile	Lys	Gln	Phe	Leu	Gln	Ser	Arg	Tyr	Leu	Glu
			85						90					95	
Lys	Pro	Met	Glu	Ile	Ala	Arg	Ile	Val	Ala	Arg	Cys	Leu	Trp	Glu	Glu
			100					105					110		
Ser	Arg	Leu	Leu	Gln	Thr	Ala	Ala	Thr	Ala	Ala	Gln	Gln	Gly	Gly	Gln
		115					120					125			
Ala	Asn	His	Pro	Thr	Ala	Ala	Val	Val	Thr	Glu	Lys	Gln	Gln	Met	Leu
		130				135					140				
Glu	Gln	His	Leu	Gln	Asp	Val	Arg	Lys	Arg	Val	Gln	Asp	Leu	Glu	Gln
	145				150					155					160
Lys	Met	Lys	Val	Val	Glu	Asn	Leu	Gln	Asp	Asp	Phe	Asp	Phe	Asn	Tyr
			165						170					175	

Lys Thr Leu Lys Ser Gln Gly Asp Met Gln Asp Leu Asn Gly Asn Asn
 180 185 190
 Gln Ser Val Thr Arg Gln Lys Met Gln Gln Leu Glu Gln Met Leu Thr
 195 200 205
 Ala Leu Asp Gln Met Arg Arg Ser Ile Val Ser Glu Leu Ala Gly Leu
 210 215 220
 Leu Ser Ala Met Glu Tyr Val Gln Lys Thr Leu Thr Asp Glu Glu Leu
 225 230 235 240
 Ala Asp Trp Lys Arg Arg Pro Glu Ile Ala Cys Ile Gly Gly Pro Pro
 245 250 255
 Asn Ile Cys Leu Asp Arg Leu Glu Asn Trp Ile Thr Ser Leu Ala Glu
 260 265 270
 Ser Gln Leu Gln Thr Arg Gln Gln Ile Lys Lys Leu Glu Glu Leu Gln
 275 280 285
 Gln Lys Val Ser Tyr Lys Gly Asp Pro Ile Val Gln His Arg Pro Met
 290 295 300
 Leu Glu Glu Arg Ile Val Glu Leu Phe Arg Asn Leu Met Lys Ser Ala
 305 310 315 320
 Phe Val Val Glu Arg Gln Pro Cys Met Pro Met His Pro Asp Arg Pro
 325 330 335
 Leu Val Ile Lys Thr Gly Val Gln Phe Thr Thr Lys Val Arg Leu Leu
 340 345 350
 Val Lys Phe Pro Glu Leu Asn Tyr Gln Leu Lys Ile Lys Val Cys Ile
 355 360 365
 Asp Lys Asp Ser Gly Asp Val Ala Ala Leu Arg Gly Ser Arg Lys Phe
 370 375 380
 Asn Ile Leu Gly Thr Asn Thr Lys Val Met Asn Met Glu Glu Ser Asn
 385 390 395 400
 Asn Gly Ser Leu Ser Ala Glu Phe Lys His Leu Thr Leu Arg Glu Gln
 405 410 415
 Arg Cys Gly Asn Gly Gly Arg Ala Asn Cys Asp Ala Ser Leu Ile Val
 420 425 430
 Thr Glu Glu Leu His Leu Ile Thr Phe Glu Thr Glu Val Tyr His Gln
 435 440 445
 Gly Leu Lys Ile Asp Leu Glu Thr His Ser Leu Pro Val Val Val Ile
 450 455 460
 Ser Asn Ile Cys Gln Met Pro Asn Ala Trp Ala Ser Ile Leu Trp Tyr
 465 470 475 480
 Asn Met Leu Thr Asn Asn Pro Lys Asn Val Asn Phe Phe Thr Lys Pro
 485 490 495
 Pro Ile Gly Thr Trp Asp Gln Val Ala Glu Val Leu Ser Trp Gln Phe
 500 505 510
 Ser Ser Thr Thr Lys Arg Gly Leu Ser Ile Glu Gln Leu Thr Thr Leu
 515 520 525
 Ala Glu Lys Leu Leu Gly Pro Gly Val Asn Tyr Ser Gly Cys Gln Ile
 530 535 540

Thr Trp Ala Lys Phe Cys Lys Glu Asn Met Ala Gly Lys Gly Phe Ser
 545 550 555 560
 Phe Trp Val Trp Leu Asp Asn Ile Ile Asp Leu Val Lys Lys Tyr Ile
 565 570 575
 Leu Ala Leu Trp Asn Glu Gly Tyr Ile Met Gly Phe Ile Ser Lys Glu
 580 585 590
 Arg Glu Arg Ala Ile Leu Ser Thr Lys Pro Pro Gly Thr Phe Leu Leu
 595 600 605
 Arg Phe Ser Glu Ser Ser Lys Glu Gly Gly Val Thr Phe Thr Trp Val
 610 615 620
 Glu Lys Asp Ile Ser Gly Lys Thr Gln Ile Gln Ser Val Glu Pro Tyr
 625 630 635 640
 Thr Lys Gln Gln Leu Asn Asn Met Ser Phe Ala Glu Ile Ile Met Gly
 645 650 655
 Tyr Lys Ile Met Asp Ala Thr Asn Ile Leu Val Ser Pro Leu Val Tyr
 660 665 670
 Leu Tyr Pro Asp Ile Pro Lys Glu Glu Ala Phe Gly Lys Tyr Cys Arg
 675 680 685
 Pro Glu Ser Gln Glu His Pro Glu Ala Asp Pro Gly Ser Ala Ala Pro
 690 695 700
 Tyr Leu Lys Thr Lys Phe Ile Cys Val Thr Pro Thr Thr Cys Ser Asn
 705 710 715 720
 Thr Ile Asp Leu Pro Met Ser Pro Arg Thr Leu Asp Ser Leu Met Gln
 725 730 735
 Phe Gly Asn Asn Gly Glu Gly Ala Glu Pro Ser Ala Gly Gly Gln Phe
 740 745 750
 Glu Ser Leu Thr Phe Asp Met Asp Leu Thr Ser Glu Cys Ala Thr Ser
 755 760 765
 Pro Met
 770

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AAYACNGARC CNATGGARAT YATT

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AAYGTNGAYC ARYTNAAYAT G

21

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

RTCDATRTTN GRGTANAR

18

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GTAYAANTYR AYCAGNGYAA

20

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GATCGAGATG TATTTCCTCAG AAAAG

25

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Leu	Asp	Gly	Pro	Lys	Gly	Thr	Gly	Tyr	Ile	Lys	Thr	Glu	Leu	Ile
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Gly	Tyr	Ile	Lys	Thr	Glu
1				5	

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Lys	Val	Asn	Leu	Gln	Glu	Arg	Arg	Lys	Tyr	Leu	Lys	His	Arg
1				5					10				

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Glu	Pro	Gln	Tyr	Glu	Glu	Ile	Pro	Ile	Tyr	Leu
1				5					10	

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vii) IMMEDIATE SOURCE:

(B) CLONE: Src

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Waksman, et al.

(C) JOURNAL: Nature
(D) VOLUME: 358
(F) PAGES: 646-653
(G) DATE: 1992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Ala	Glu	Glu	Trp	Tyr	Phe	Gly	Lys	Ile	Thr	Arg	Arg	Glu	Ser	Glu	Arg	
1				5					10					15		
Leu	Leu	Leu	Asn	Pro	Glu	Asn	Pro	Arg	Gly	Thr	Phe	Leu	Val	Arg	Glu	
			20					25					30			
Ser	Glu	Thr	Thr	Lys	Gly	Ala	Tyr	Cys	Leu	Ser	Val	Ser	Asp	Phe	Phe	
		35					40					45				
Asp	Asn	Ala	Lys	Gly	Leu	Asn	Val	Lys	His	Tyr	Lys	Ile	Arg	Lys	Leu	
	50					55						60				
Asp	Ser	Gly	Gly	Phe	Tyr	Ile	Thr	Ser	Arg	Thr	Gln	Phe	Ser	Ser	Leu	
65					70					75					80	
Gln	Gln	Leu	Val	Ala	Tyr	Tyr	Ser	Lys	His	Ala	Asp	Gly	Leu	Cys	His	
				85					90					95		
Arg	Leu	Thr	Asn	Val	Cys	Pro	Thr	Ser								
			100					105								

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 99 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vii) IMMEDIATE SOURCE:
(B) CLONE: Abl

(x) PUBLICATION INFORMATION:
(A) AUTHORS: Overduin, et al.
(C) JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
(D) VOLUME: 89
(F) PAGES: 11673-11677
(G) DATE: 1992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Glu	Lys	His	Ser	Trp	Tyr	His	Gly	Pro	Val	Ser	Arg	Asn	Ala	Ala	Glu	
1				5					10					15		
Tyr	Leu	Leu	Ser	Ser	Gly	Ile	Asn	Gly	Ser	Phe	Leu	Val	Arg	Glu	Ser	
			20					25					30			
Asp	Arg	Arg	Pro	Gly	Gln	Arg	Ser	Ile	Ser	Leu	Arg	Tyr	Glu	Glu	Gly	
		35					40					45				
Arg	Val	Tyr	His	Tyr	Arg	Ile	Asn	Thr	Ala	Ser	Asp	Gly	Lys	Leu	Tyr	
	50					55					60					

Val Ser Ser Glu Ser Arg Phe Asn Thr Leu Ala Glu Leu Val His His
65 70 75 80
His Ser Thr Val Ala Asp Gly Leu Ile Thr Thr Leu His Tyr Pro Ala
85 90 95
Pro Lys Arg

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: Lck
- (x) PUBLICATION INFORMATION:
 - (A) AUTHORS: Eck, et al.
 - (C) JOURNAL: Nature
 - (D) VOLUME: 362
 - (F) PAGES: 87-91
 - (G) DATE: 1993
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Trp Phe Phe Lys Asn Leu Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu
1 5 10 15
Ala Pro Gly Asn Thr His Gly Ser Phe Leu Ile Arg Glu Ser Glu Ser
20 25 30
Thr Ala Gly Ser Phe Ser Leu Ser Val Arg Asp Asp Phe Asp Gln Asn
35 40 45
Gln Gly Glu Val Val Lys His Tyr Lys Ile Arg Asn Leu Asp Asn Gly
50 55 60
Gly Phe Tyr Ile Ser Pro Arg Ile Thr Phe Pro Gly Leu His Asp Leu
65 70 75 80
Val Arg His Tyr Thr Asn Ala Ser Asp Gly Leu Cys Thr Arg Leu Ser
85 90 95
Arg Pro Cys Gln Thr Gln
100

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 99 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (v) FRAGMENT TYPE: internal
 (vii) IMMEDIATE SOURCE:
 (B) CLONE: p85[alpha]N

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Gln	Asp	Ala	Glu	Trp	Tyr	Trp	Gly	Asp	Ile	Ser	Arg	Glu	Glu	Val	Asn	1	5	10	15
Glu	Lys	Leu	Arg	Asp	Thr	Ala	Asp	Gly	Thr	Phe	Leu	Val	Arg	Asp	Ala	20	25	30	
Ser	Thr	Lys	Met	His	Gly	Asp	Tyr	Thr	Leu	Thr	Leu	Arg	Lys	Gly	Gly	35	40	45	
Asn	Asn	Lys	Leu	Ile	Lys	Ile	Phe	His	Arg	Asp	Gly	Lys	Tyr	Gly	Phe	50	55	60	
Ser	Asp	Pro	Leu	Thr	Phe	Asn	Ser	Val	Val	Glu	Leu	Ile	Asn	His	Tyr	65	70	75	80
Arg	His	Glu	Ser	Leu	Ala	Gln	Tyr	Asn	Pro	Lys	Leu	Asp	Val	Lys	Leu	85	90	95	
Leu	Tyr	Pro																	